

FIGURE 1A

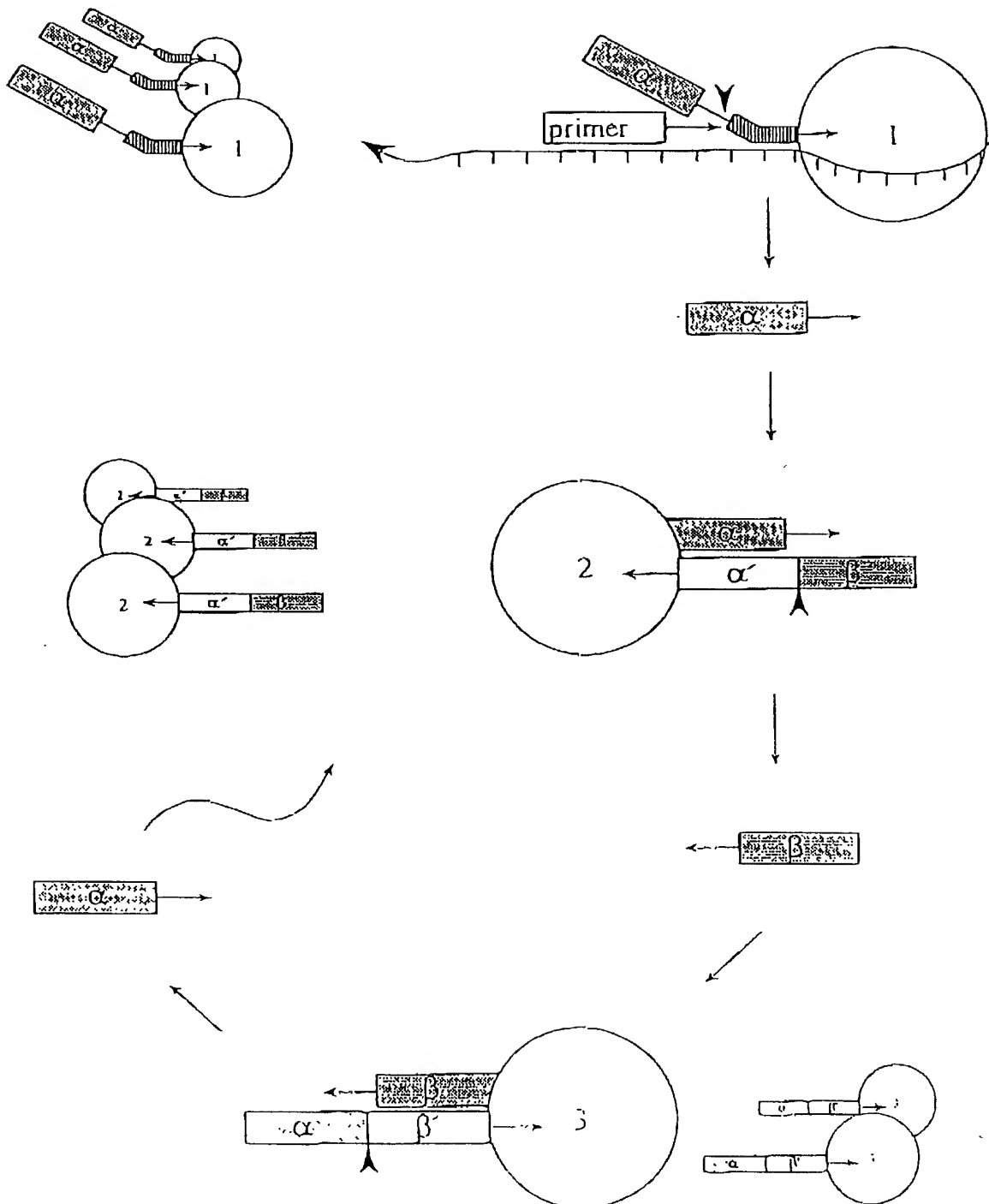
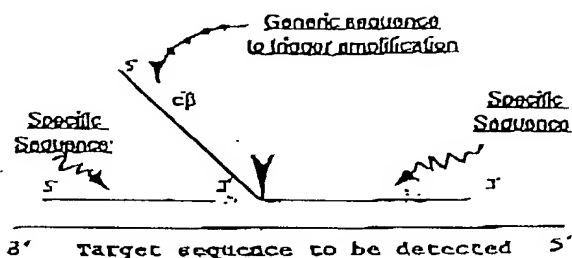


FIGURE 1B

PART ONE: TRIGGER REACTION



PART TWO: DETECTION REACTION

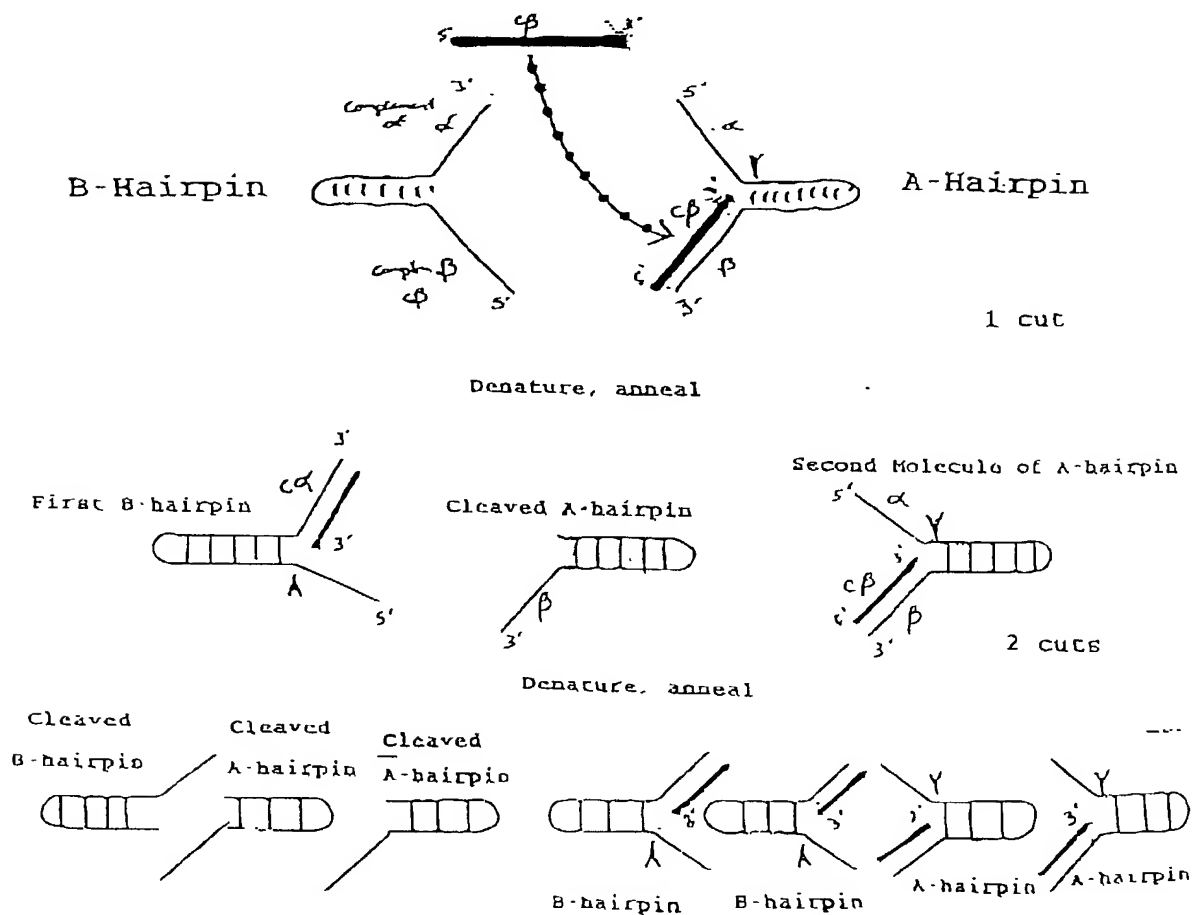


FIGURE 2 (cont'd)

MAJORITY (SEQ ID NO:7)	CCAGCCCGCAGCAGCCTXCTGCGCCACCGCTGGCCAAAGCGCGCAAAACGAGGGGCIACGAGGTCGGGCAICCTC	
DNAPTAA (SEQ ID NO:1)C.....G.....C.....C.....	417
DNAPTFL (SEQ ID NO:2)G.....CG.....	414
DNAPTH (SEQ ID NO:3)T.....C.....	420
MAJORITY	ACCGCCCGCAGCAGCCTGACGAGCCTCTTCCGACCGGCAICCGGCTGCTCCAGCCCGGACGGGCIACGCTCA	
DNAPTAA (SEQ ID NO:1)AAA.....T.....CA.....	487
DNAPTFL (SEQ ID NO:2)T.....G.....G.....A.....T.....G.....	484
DNAPTH (SEQ ID NO:3)A.....G.....G.....G.....CC.....	490
MAJORITY	TCAGCCCGCGGCTGCTTCCGACAGCTACCGGCTGAGCGCGCGGAGCACTGGGTGGACTACCGCGGCGGCTCGG	
DNAPTAA (SEQ ID NO:1)C.....A.....C.....C.....CC.....A.....	557
DNAPTFL (SEQ ID NO:2)AC.....AC.....C.....C.....	554
DNAPTH (SEQ ID NO:3)A.....A.....C.....C.....T.....C.....T.....	560
MAJORITY	CGCGGACCGCTCGGACCAACCTCGCGCGGCTCAAGCGGCAICCGCGGACAAAGCGGCGGCGGCAAGCTCGCTCXAG	
DNAPTAA (SEQ ID NO:1)GAG.....T.....G.....GAG.....T.....GG.....	627
DNAPTFL (SEQ ID NO:2)G.....I.....A.....G.....A.....G.....A.....CGG.....	624
DNAPTH (SEQ ID NO:3)G.....I.....A.....G.....T.....G.....A.....	630
MAJORITY	GAGTCGGCGCAGCGCTGGAAAGCCTGCTCAAGAACCTGGACCGGCTCAAGCGCGGCGGCGGCGGCGGCAAGCA	
DNAPTAA (SEQ ID NO:1)CC.....CC.....C.....A.....	694
DNAPTFL (SEQ ID NO:2)I.....G.....C.....A.....T.....T.....C.....C.....	691
DNAPTH (SEQ ID NO:3)A.....A.....A.....A.....A.....A.....A.....C.....	700

FIGURE 2 (cont'd)

[illegible]

FIGURE 2 (cont'd)

HAJORITY	(SEQ ID NO:7)	ACAACATCGCGGCGCCACCCXCTGCCCCAGAGCGATCGCGCGGGCGTTCGCGCGGAGGCGXCGCGT	
DNAPTAG	(SEQ ID NO:1)G..T..G.....A..C.....C...C..	1814
DNAPTR	(SEQ ID NO:2)G.....T.....C..C.....A.....C.....C.....	1811
DNAPTH	(SEQ ID NO:3)G.....G.....C.....C.....C.....T.....C..	182
HAJORITY		GTTCGCGCGCGGCGGATAGAGGTCGCGGTCGCGCGGACCGTCTCGCGGAGGAGACCGTC	
DNAPTAG		A.....T.....A.....G.....C.....C.....	1884
DNAPTR	T.....T.....T.....C.....A.....A.....	1881
DNAPTH	T.....T.....T.....C.....C.....A.....	1890
HAJORITY		ATCGCGGCGTTCGAGAGCGGAGGACATCCAGAGCGGCGGAGCGTGGATGTCGCGGTCGCGCGG	
DNAPTAG	G.....G.....G.....G.....G.....G.....	1954
DNAPTR	T.....T.....T.....T.....T.....T.....	1951
DNAPTH	A.....A.....A.....A.....A.....A.....	1960
HAJORITY		AGCGCGTTCGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	
DNAPTAG	A.....A.....A.....A.....A.....A.....	201
DNAPTR	A.....A.....A.....A.....A.....A.....	2021
DNAPTH	A.....A.....A.....A.....A.....A.....	2030
HAJORITY		CCAGCGCGGTCGCGGAGGCGTTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGG	
DNAPTAG	A.....A.....A.....A.....A.....A.....	2094
DNAPTR	G.....G.....G.....G.....G.....G.....	2091
DNAPTH	TA..G.....T.....T.....T.....T.....A.....	2100

8

FIGURE 2 (cont'd)

MAJORITY (SEQ ID NO:7)	ACCCTCCCAAGCTCGGGGCGCTGCATTGACAAAGACCCCTGCAGCAGGCGCAGCGCGCGGCTACCTCCACA	2164
CHAPTAD (SEQ ID NO:1)	2161
CHAPTAL (SEQ ID NO:2)	217
CHAPTH (SEQ ID NO:3)	
MAJORITY	CCGTCCTCCGCGCGCGCGCTACCTCGCGGACCTCAACCGCGCGCTCAACGCTCGCGGACGCGCGCGG	2234
CHAPTAD	2231
CHAPTAL	2240
CHAPTH	
MAJORITY	CGGCATCGCCCTCAACATCGCGCTCCAGCGCGCGCGCGCGCGCTCATCAAGCTGGCGATCGTCAAGCTC	2304
CHAPTAD	2301
CHAPTAL	2310
CHAPTH	
MAJORITY	TTCCCGCGCGCTXCAGGAAATCGCGCGCGCGCGCGCGCTCCCTCCCTCCAGCGCGCGCGCGCGCG	2371
CHAPTAD	2371
CHAPTAL	2380
CHAPTH	
MAJORITY	CCAAACACCGCGCGCGCGCGCTGGCGCGCTTCCCGCGCGCGCGCGCGCTGATCGAGCGCGCGCTATCGCGCGCG	2444
CHAPTAD	2441
CHAPTAL	2450
CHAPTH	

FIGURE 2 (cont'd)

MAJORITY	(SEQ ID NO:7)	CCCCC CCAGG CCAGG CGGCGATCGGCGATCGGCGAAGGACTCGCTCTCGGCGCAAGGAGTAC	2499
CHAPTAN	(SEQ ID NO:1)A.....	2496
CHAPTIC	(SEQ ID NO:2)GC.....	2505
CHAPTIX	(SEQ ID NO:3)[.....	

FIGURE 3 (cont'd)

MAJORITY (SEQ ID NO:8)	AGLLAXOLAVLALREGLQXPCDDPHL LAYLLOPSNTTPEGVARRYGCWTFEDAGERALLSERLFXNLXX	
1A0 PRO (SEQ ID NO:4)	S.....G.P.....E.....A.....A.....WG	488
1L PRO (SEQ ID NO:5)	I.....F.E.....A.....OT,KE	487
1TH PRO (SEQ ID NO:6)	S.....V.....AH.....HR..LK 420	490
MAJORITY	RIEGEERLLWLYXEVEKPLSRVLAHMEATGVRLDVAYLQALSLEVAEEI RRLSEEVRACHPFNLNSAO	
1A0 PRO	R...R...A...A.....R.....A.....A.....	488
1L PRO	E.....R.....EA,V.O.....	487
1TH PRO	K.....H.....L.....	490
MAJORITY	OLERVLFDELGLPAICKIEKTGXASTSAAVLEALREAHPIVEKILQYRELTKLKNTYIDPLPLVHPRTG	
1A0 PROS.....D.I.....	558
1L PRODR.....A.....K...	557
1TH PRO	A...L...O.....H.....V.....S.....	560
MAJORITY	RLHTRFNOJATATGALSSSDPHLQHPVATPLGQRI RRAFFVAEEGWXLVALDYSOIELRVLAHLSCDNL	
1A0 PROI.....L.....	628
1L PROV..V.....	627
1TH PROA..A.....	630
MAJORITY	I AVFOECROJHTQTASWMFQVPPPEAVDPLHARA AKTIHFGVLVGMASHALSDLAIPYEEAVAFIERYFO	
1A0 PRO	E.....R.....O.....	698
1L PRO	S..G.....C..S.....	697
1TH PRO	K.....V.....	700

FIGURE 3 (cont'd)

MAJORITY (SEQ ID NO:3)	SFPKVRAWI	ENTLEECARRRGYVETLFCARRYPDLNAAVKSVREAAERMAFNMPVQOTAAADLWKLAMVXL	760
1A0 PR0 (SEQ ID NO:4)		E.....	767
TR PR0 (SEQ ID NO:5)		G.....	770
TTX PR0 (SEQ ID NO:6)		K.....	
MAJORITY	FPRLXEMGAARMLOVHDELVL	EAPKXRAEXXVAALAKEVMEGVYPLAVPLEVEVXGEOWLSAKEX	
1A0 PR0	E.....	E...A...R.....	833
TR PR0	O...L.....	D...R.....W...O.....	831
TTX PR0	R.....	QA...L...A...KA.....H.....G	835

FIGURE 4

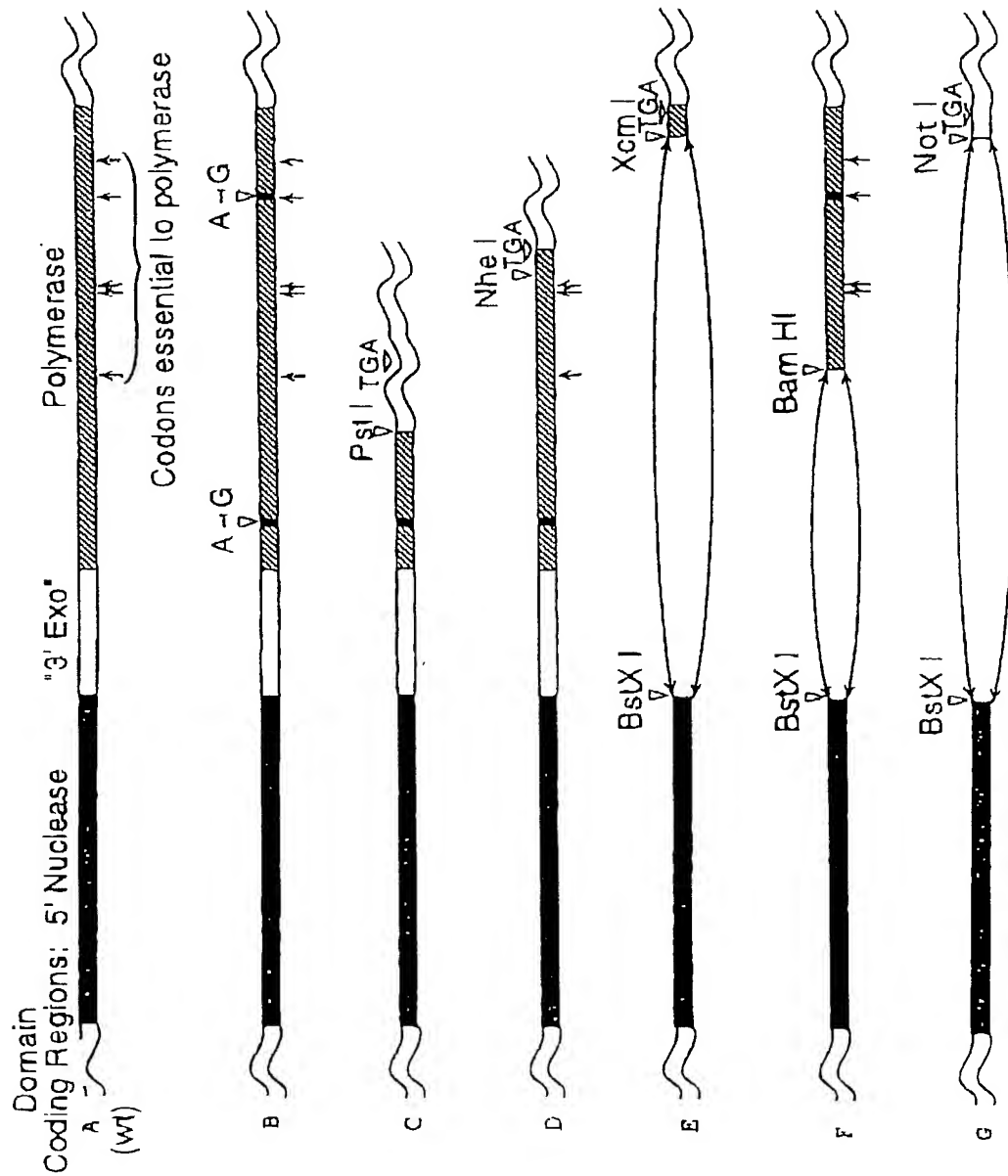


FIGURE 5

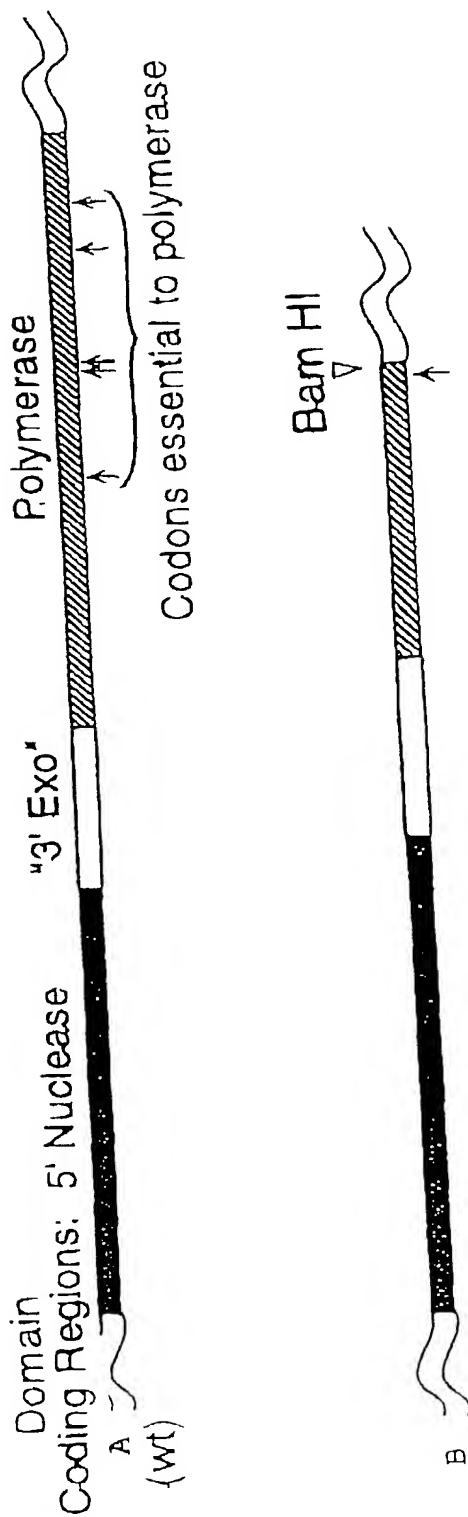
Genes for Wild-Type and Pol(-) DNAPT^H

FIGURE 6

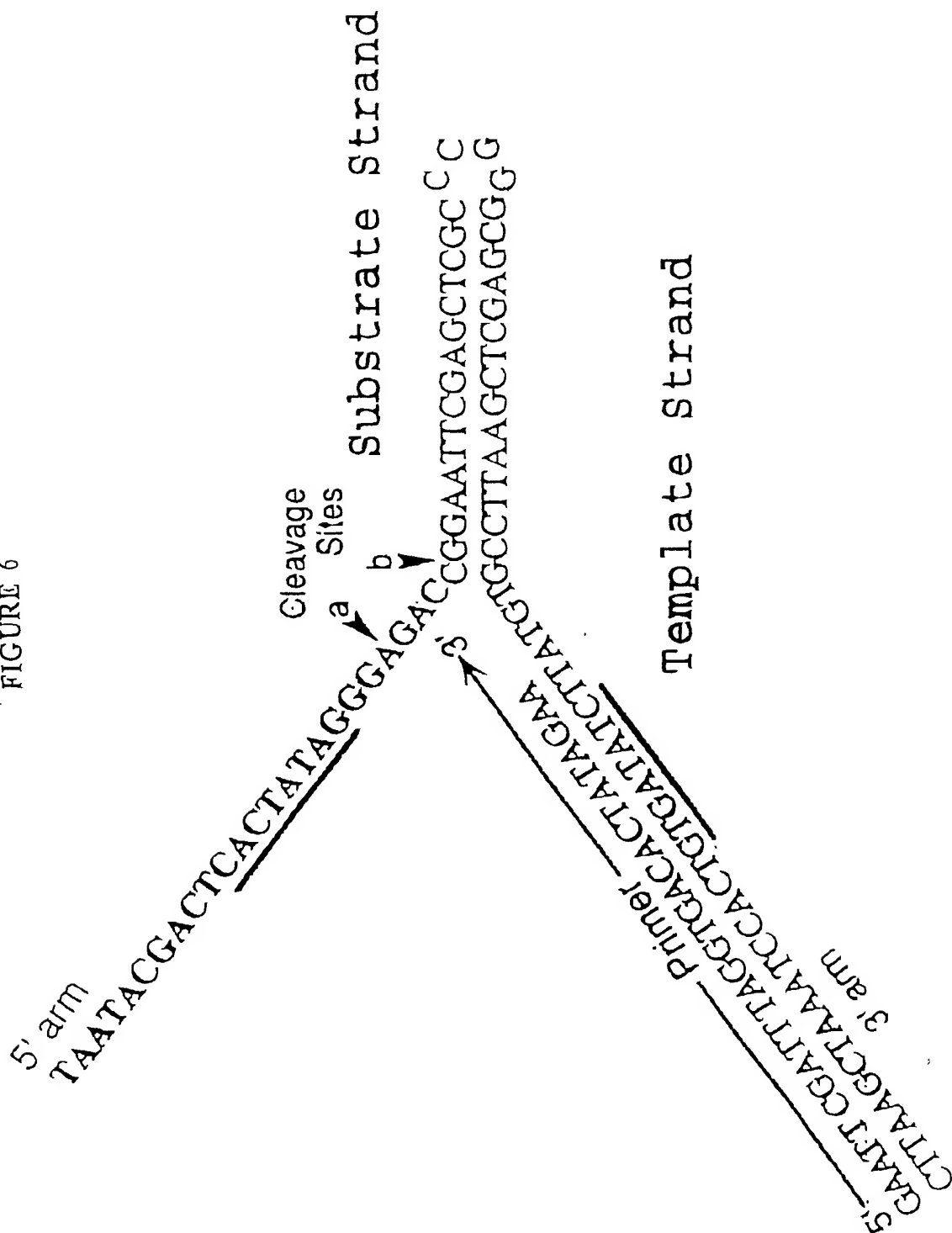


FIGURE 7

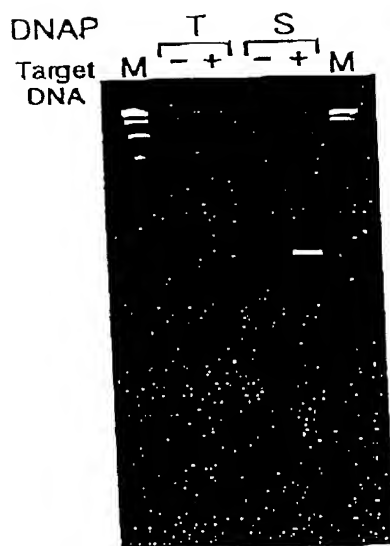


FIGURE 8

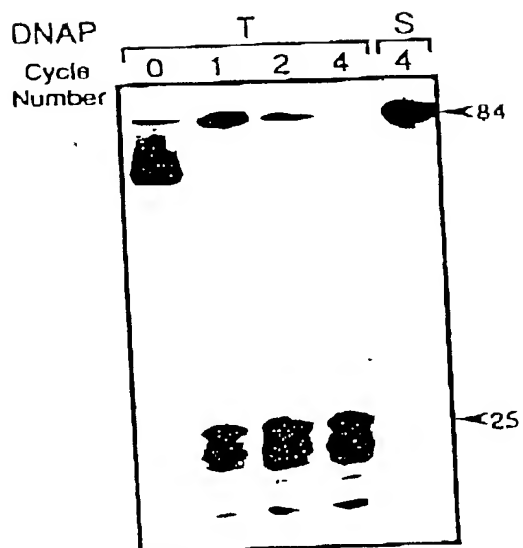


FIGURE 9

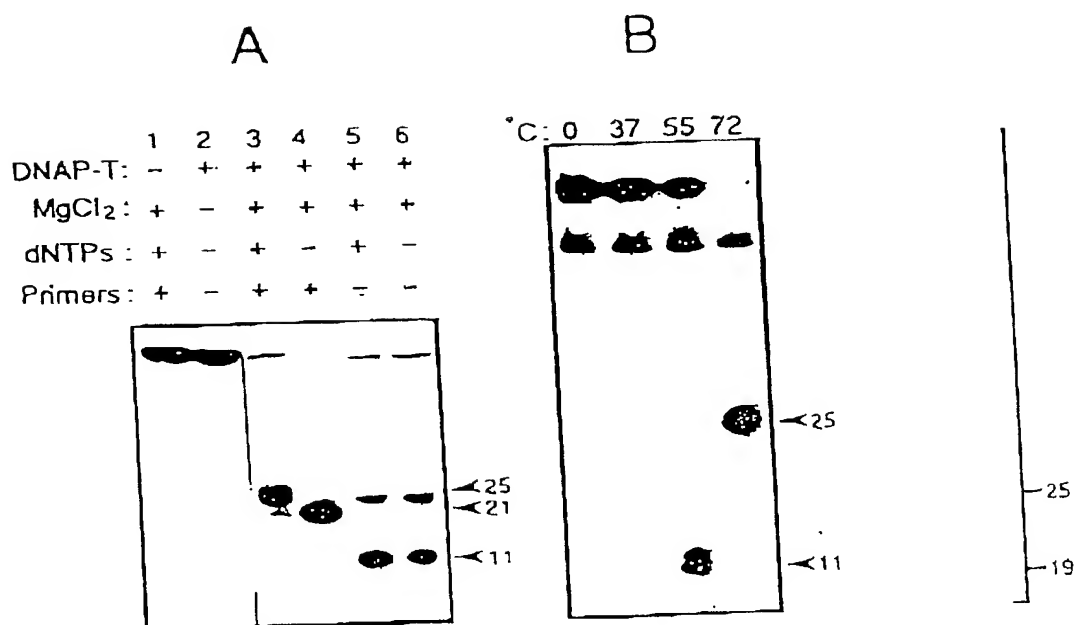


FIGURE 10

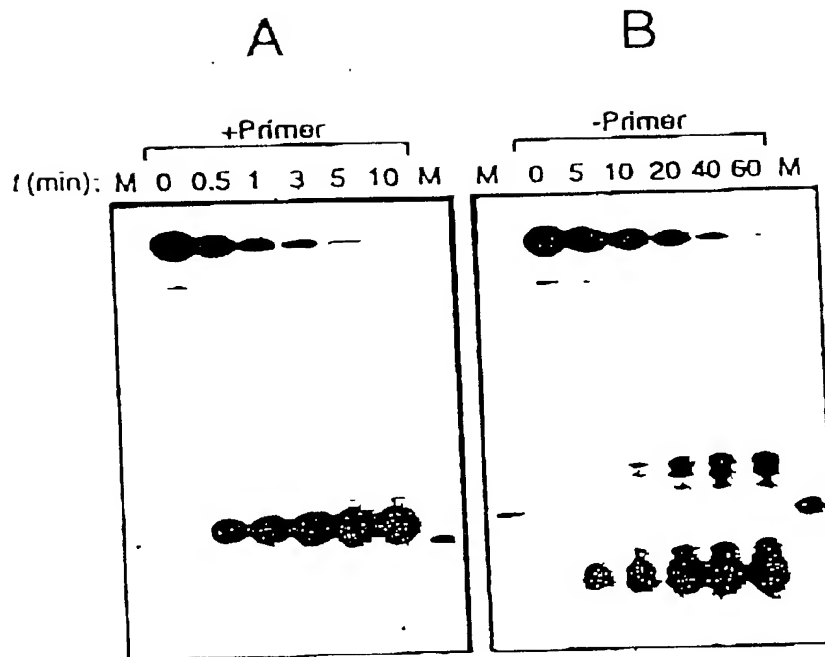


FIGURE 11

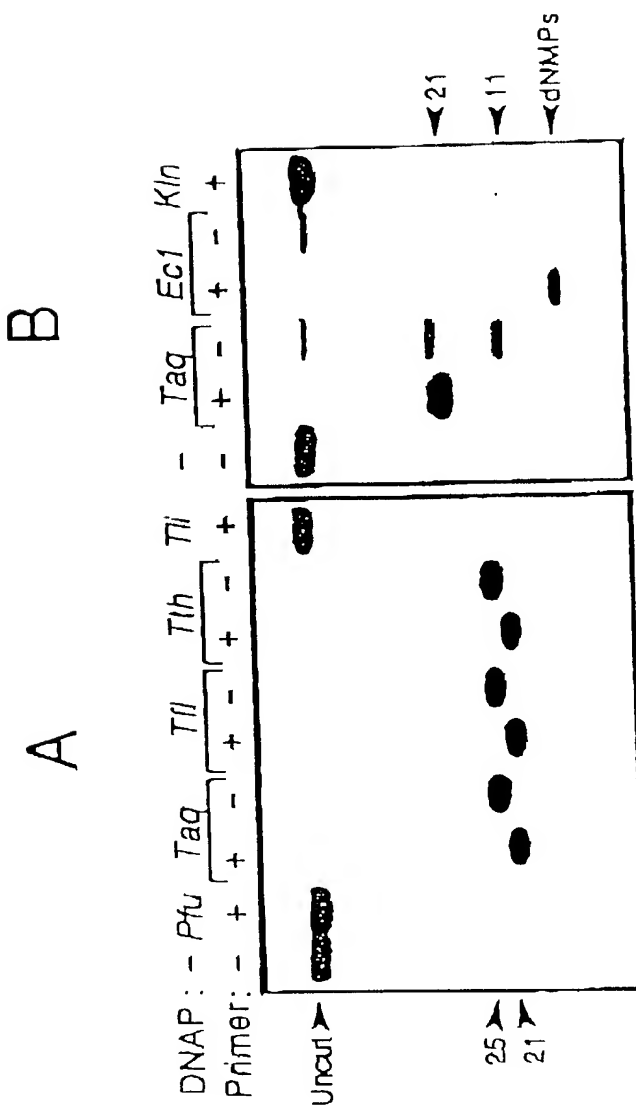


FIGURE 12

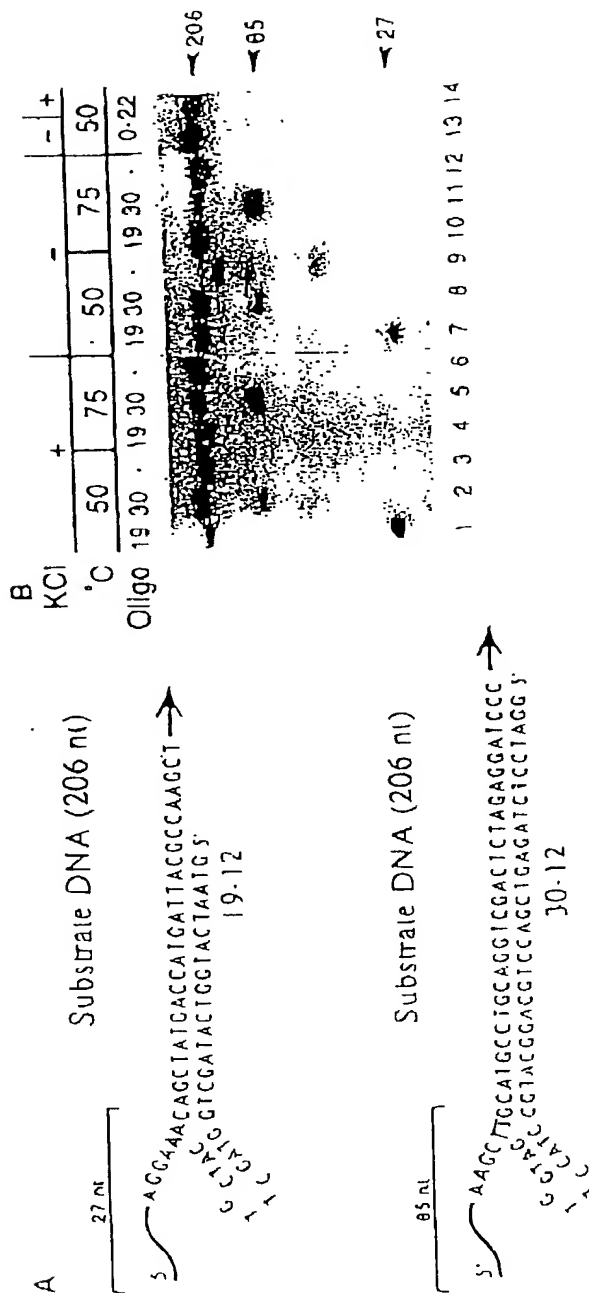


FIGURE 13

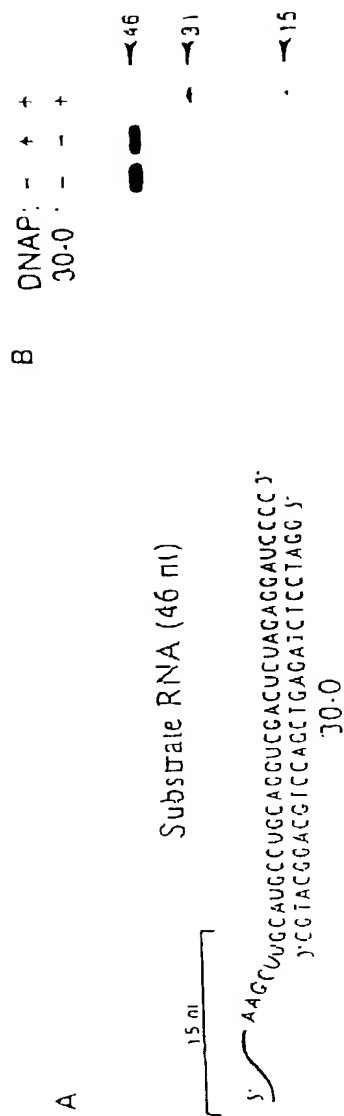


FIGURE 14

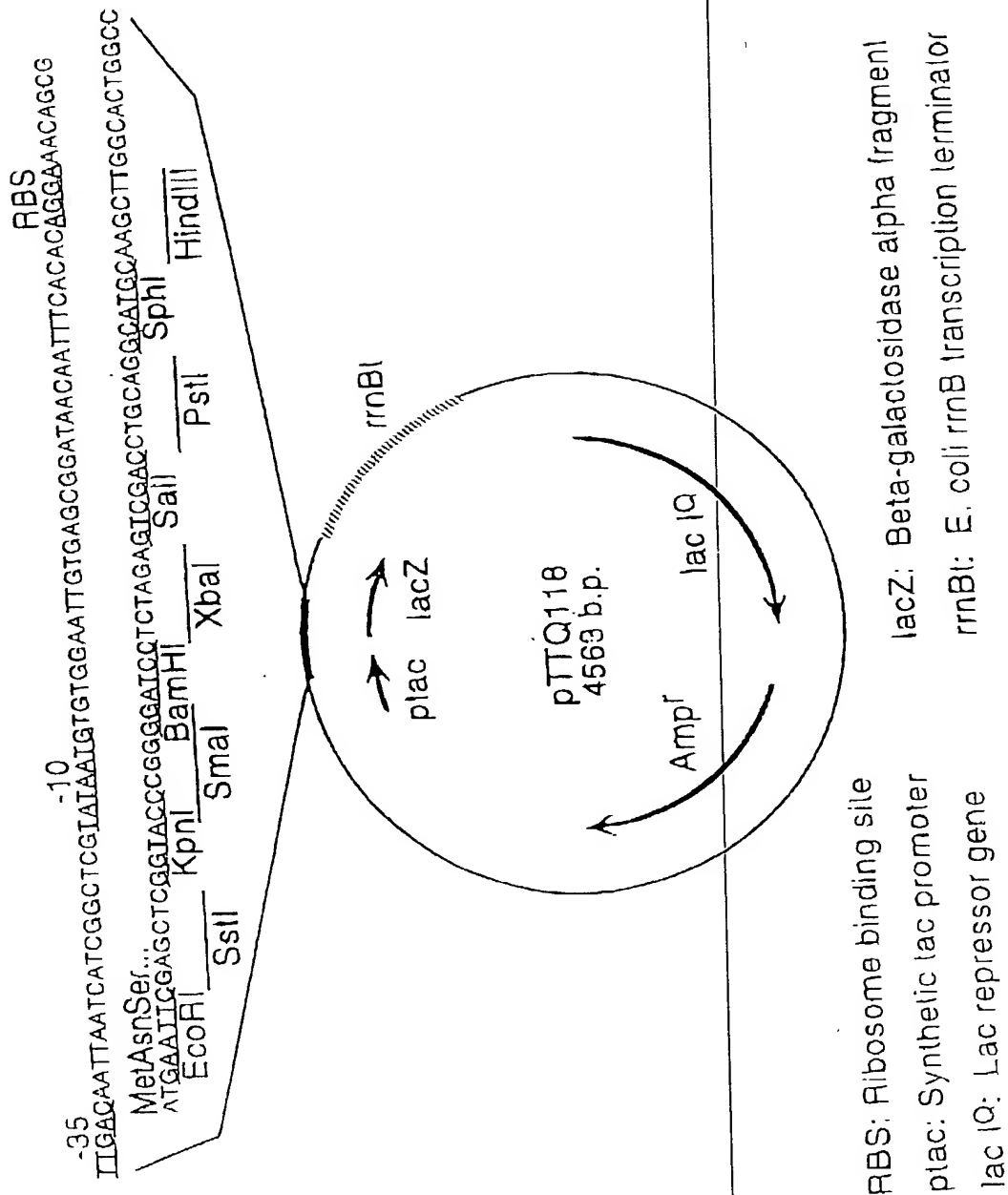


FIGURE 16

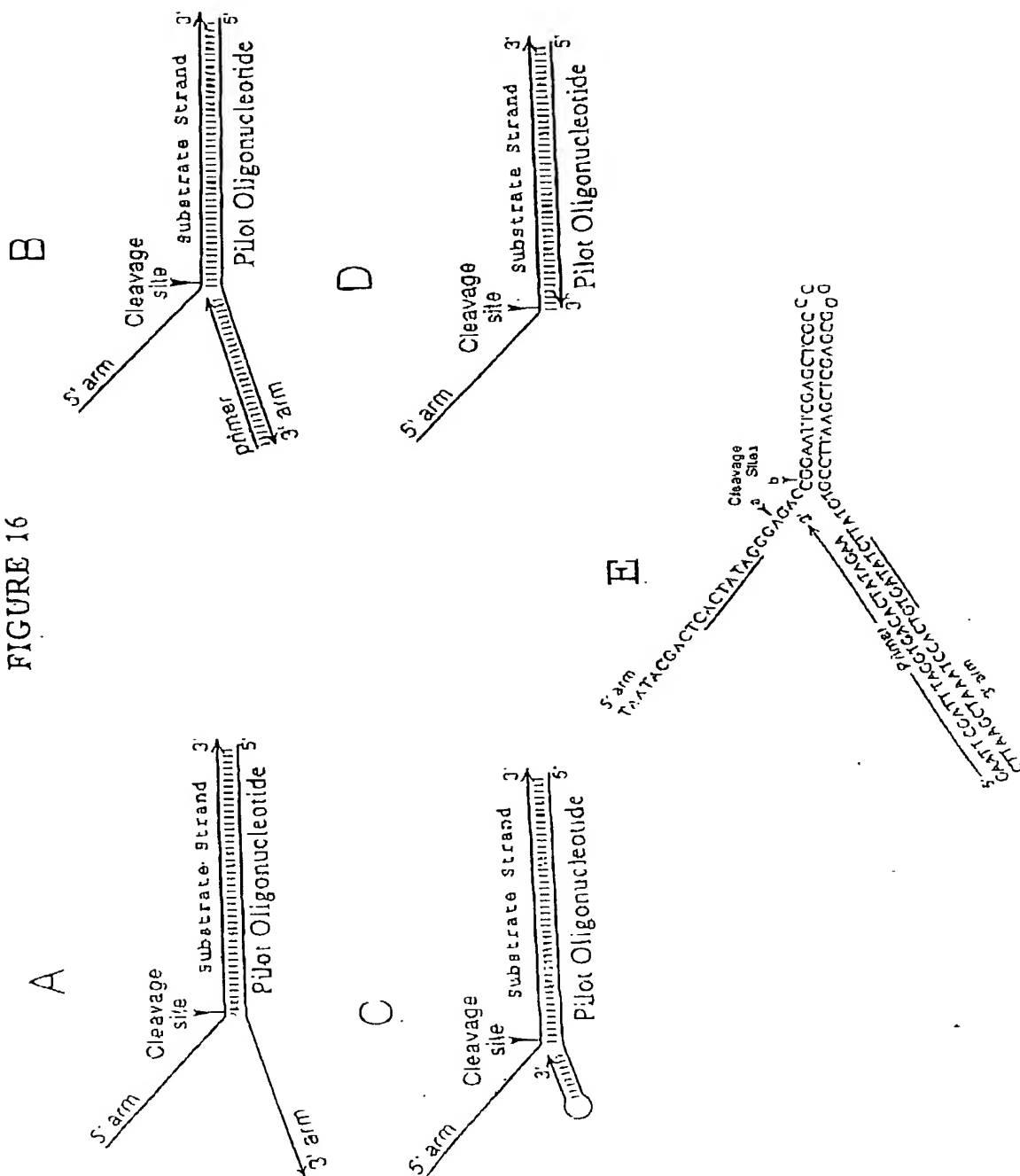


FIGURE 17

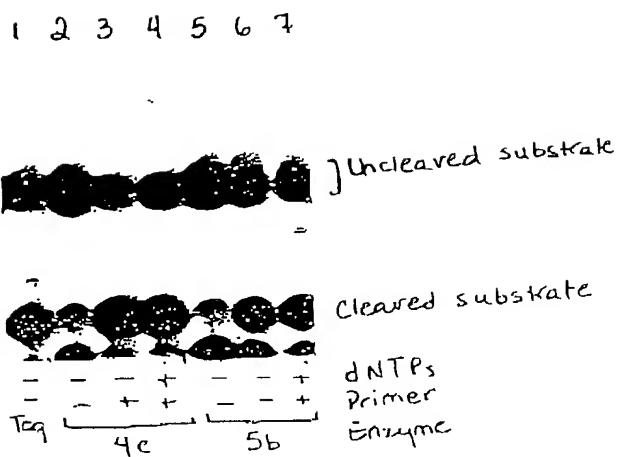
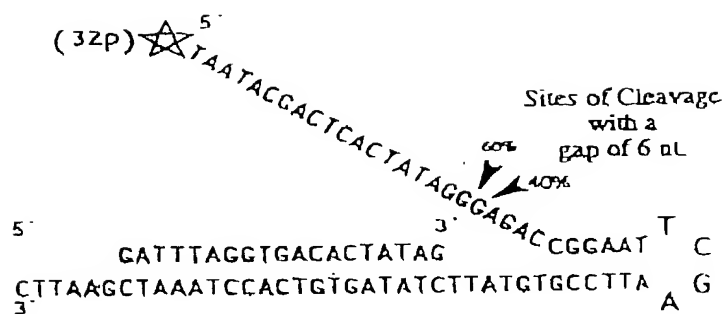


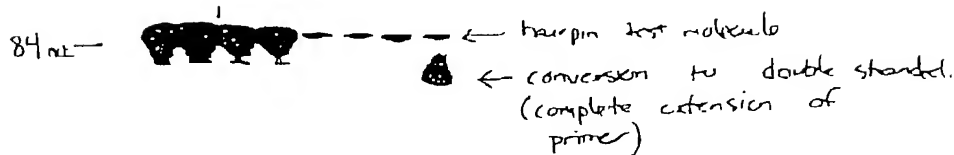
FIGURE 19

A

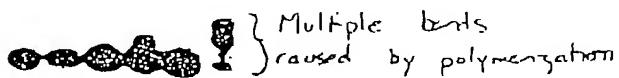


B

		"4d"		"4b"			
		No mutation		(2 pr. small activity)		Unmodified DNAP Tag	
		Rel. Activity		Rel. Activity			
1	2	3	4	5	6	7	8
		C ⁺		T ⁺		T ⁺	
		+		+		+	



desired product →
 21 nuc.



↑ some aberrant cleavage with 4b" because of residual polymerase activity.

A

5'
 --CGGACGAACAAGCGACACACCGACACAGI A
 GTACC C
 CATGG A
 T

"Tau"
 CAAAGACg=cACAgCagAgAgAAACGGAGAA-
 3'

A-Hairpin

Predicted cleavage sites

5' GTTCTCccgTCTcCTcTcTCTTCTCTT! A
 GTACC T
 CATGG C
 T

"Alpha"
 ---CTcCTTcTTCcTCTcTcCCcTGTGTC-
 3'

T-Hairpin

Sequence of alpha primer:

5' GAC GAA CAA CCG AGA CAG CC 3'

C

Top = T-Hairpin
 Bottom = A-Hairpin

Restriction sites (from left to right):
 BsmAI, RsaI, MnlI, NlaIII, HgiC I, NlaIV, RsaI, KpnI, BsmAI

DNA sequence (5' to 3'): GTTCTGCTGTCCTCTCTCTGCGCTTTGACCATGTGGTACCTGTGTCGCTGTCCTGCTTCTGCTC

FIGURE 21

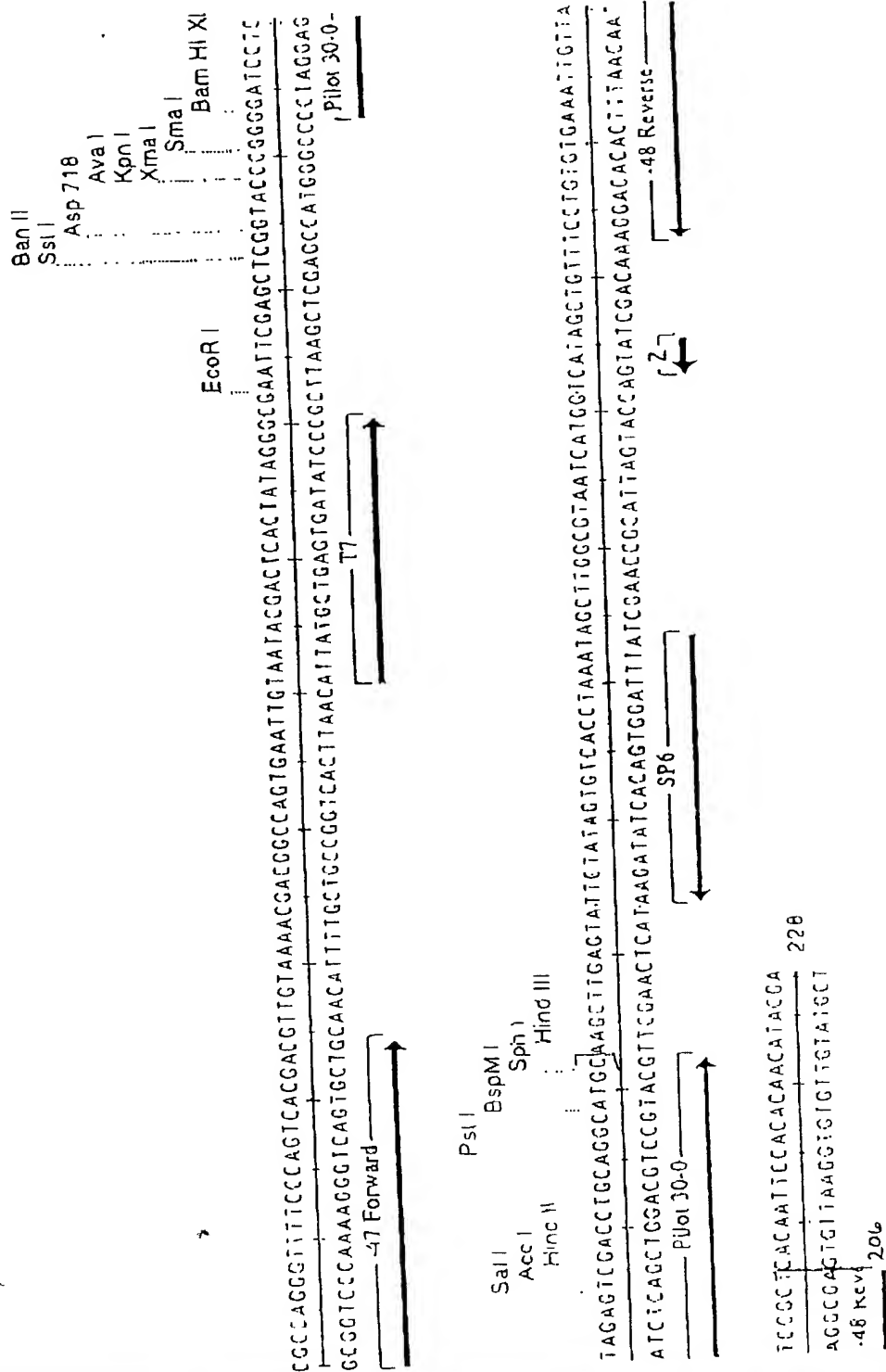


FIGURE 22A

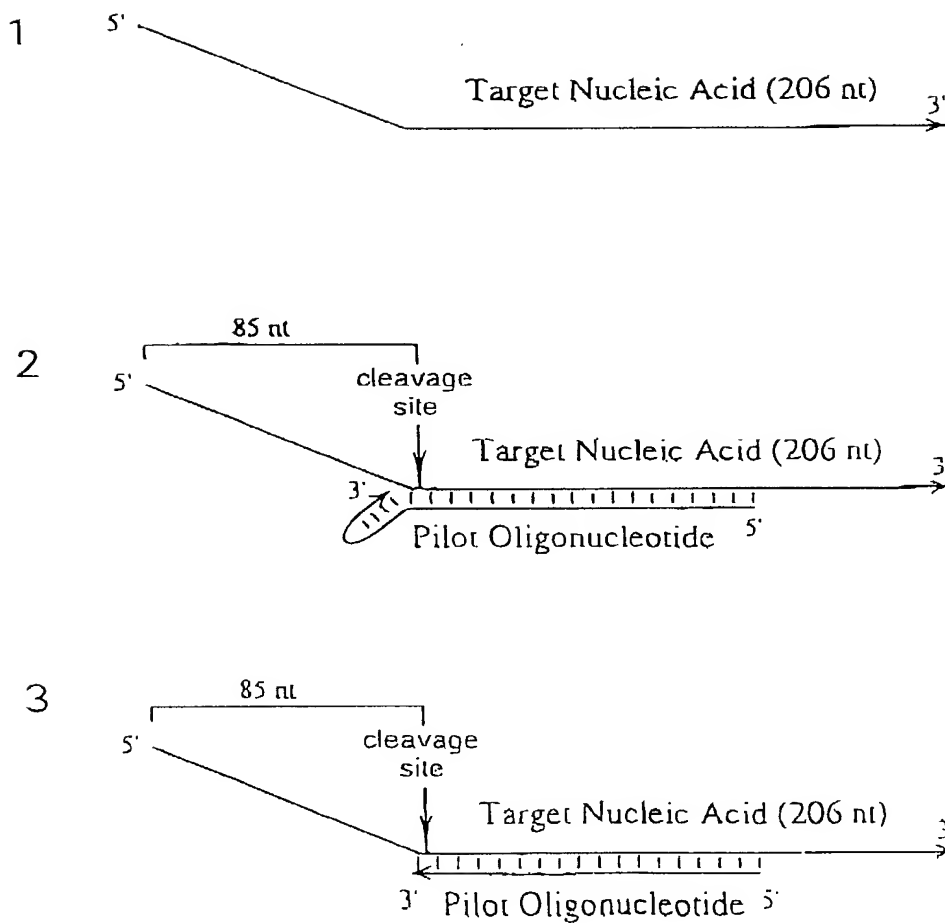


FIGURE 22B

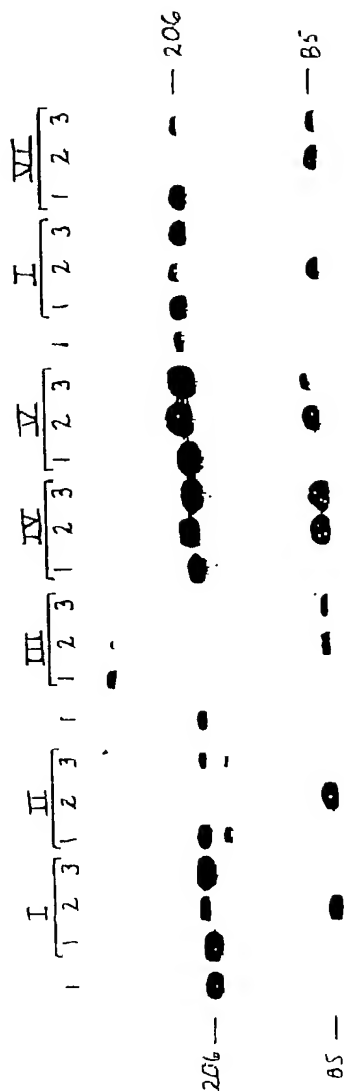


FIGURE 23

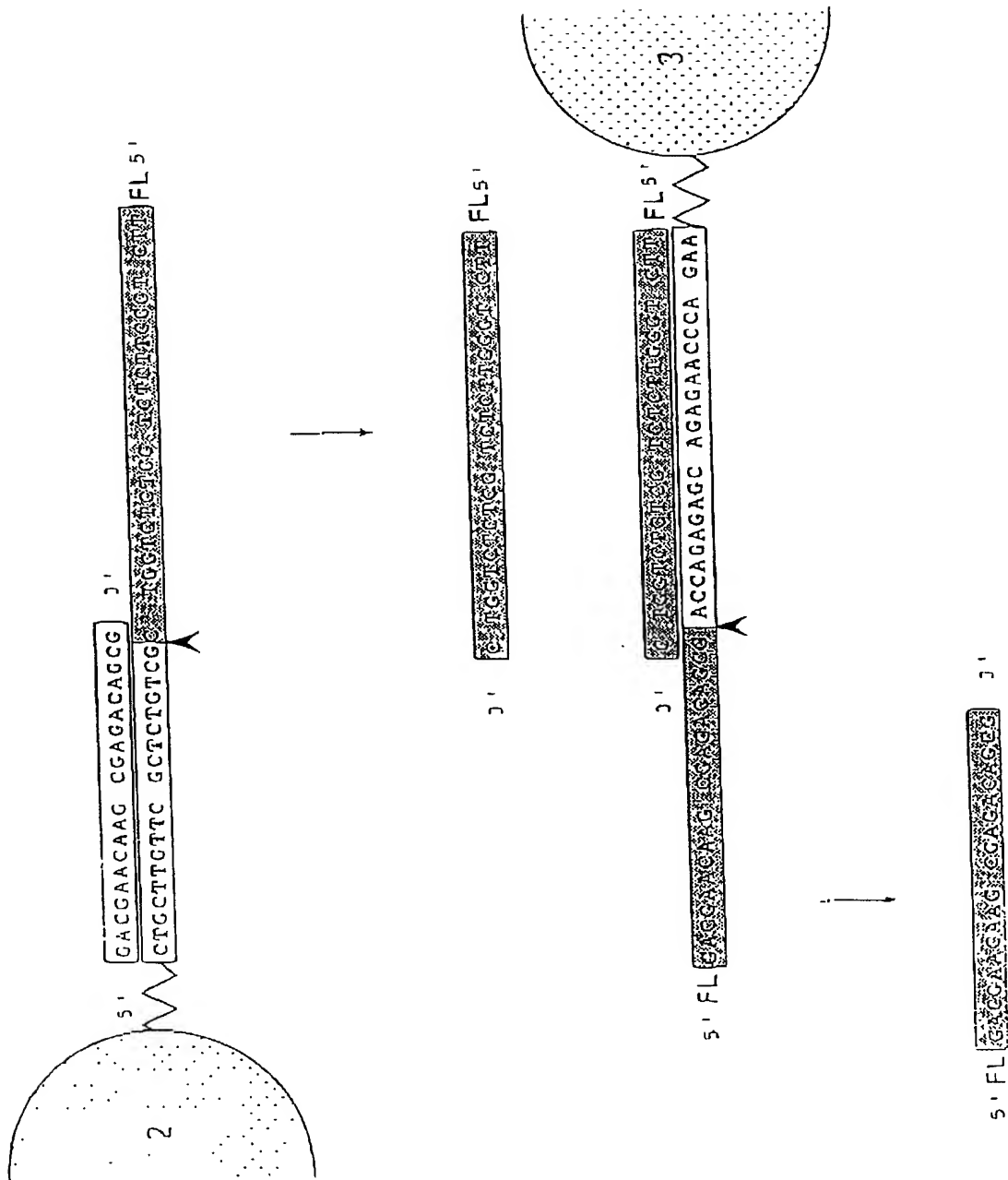


FIGURE 25

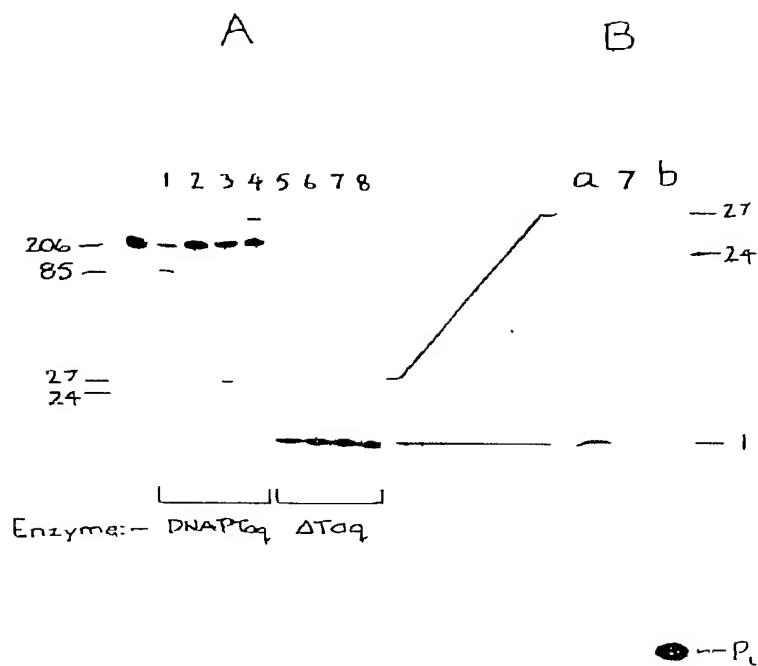
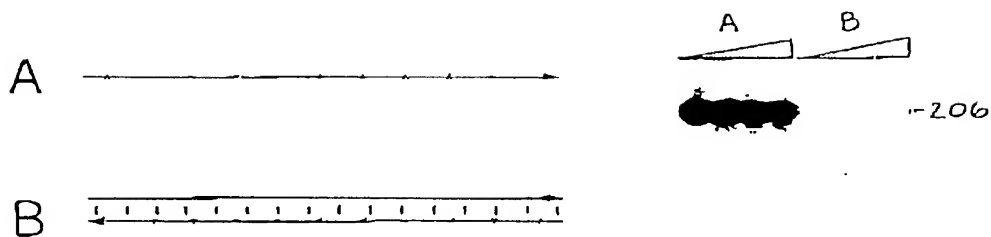


FIGURE 26



$\cdot = {}^{32}\text{P}$

FIGURE 27

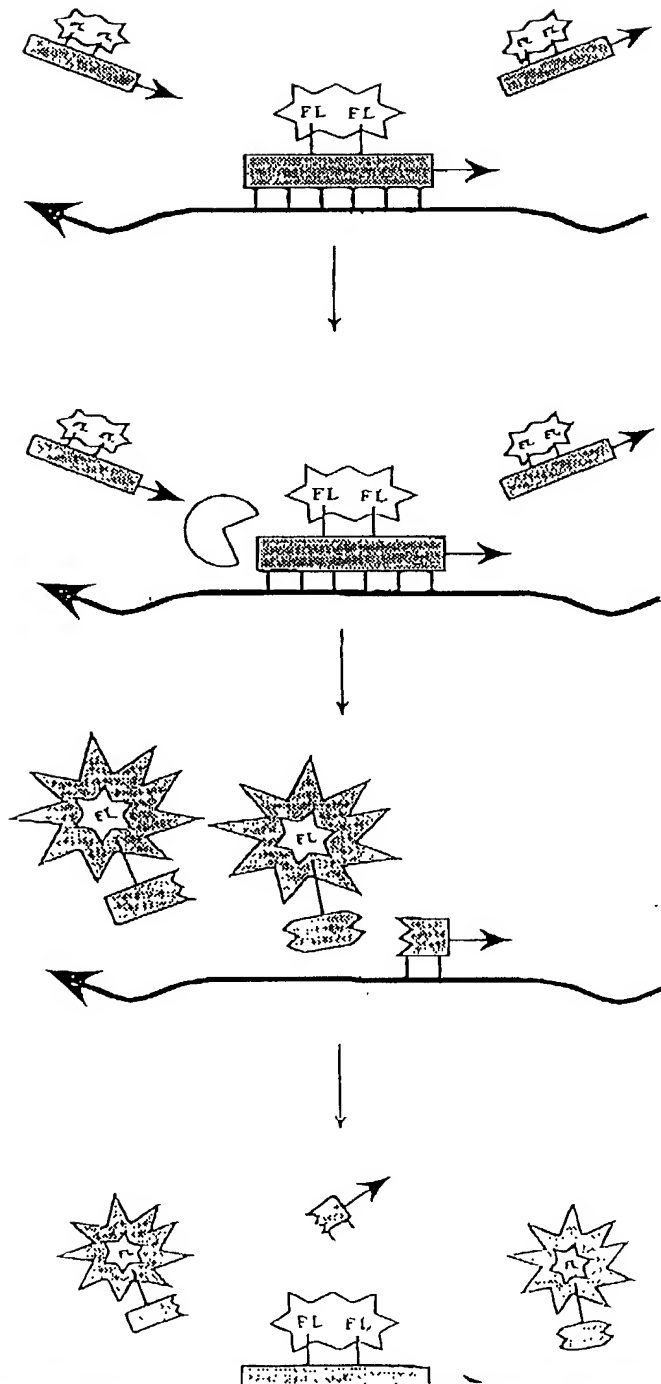
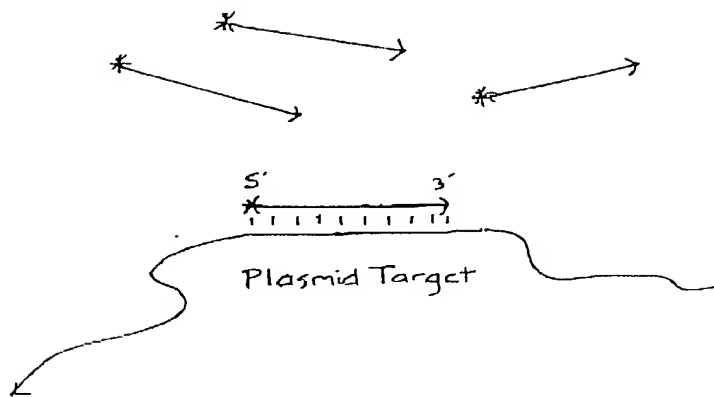
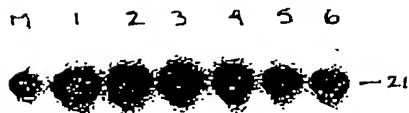


FIGURE 28A



* = ^{32}P 5' terminal phosphate

FIGURE 28B



-1

FIGURE 29

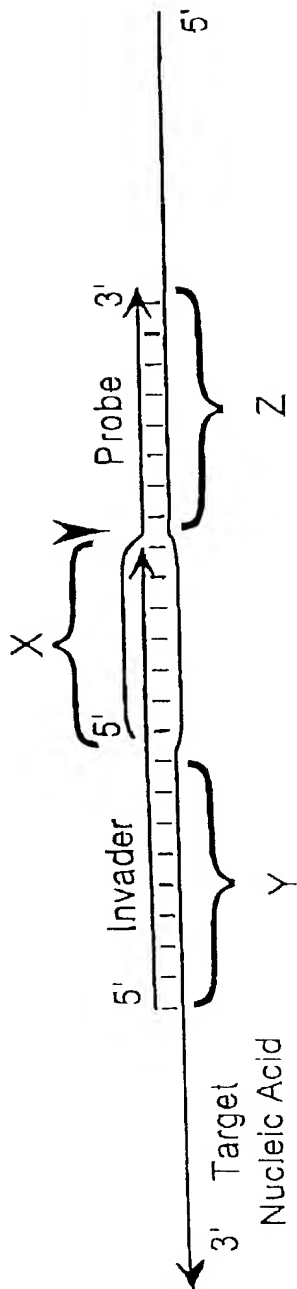


FIGURE 30

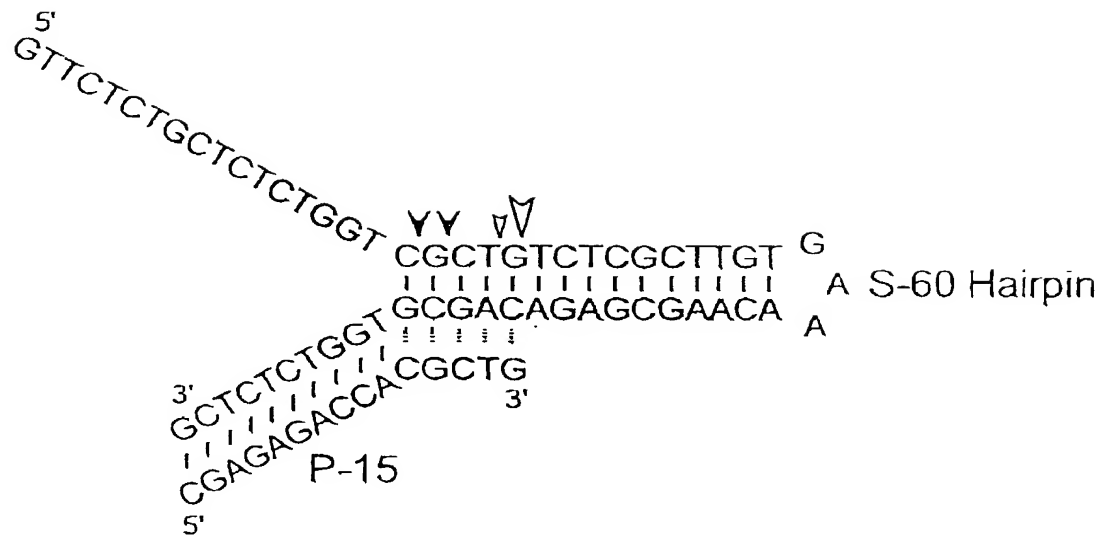
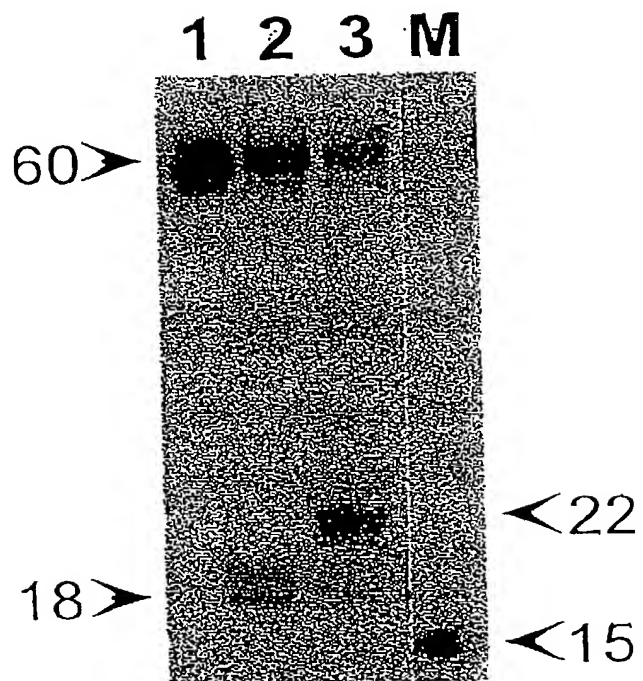


FIGURE 31



4

9

5

4

3

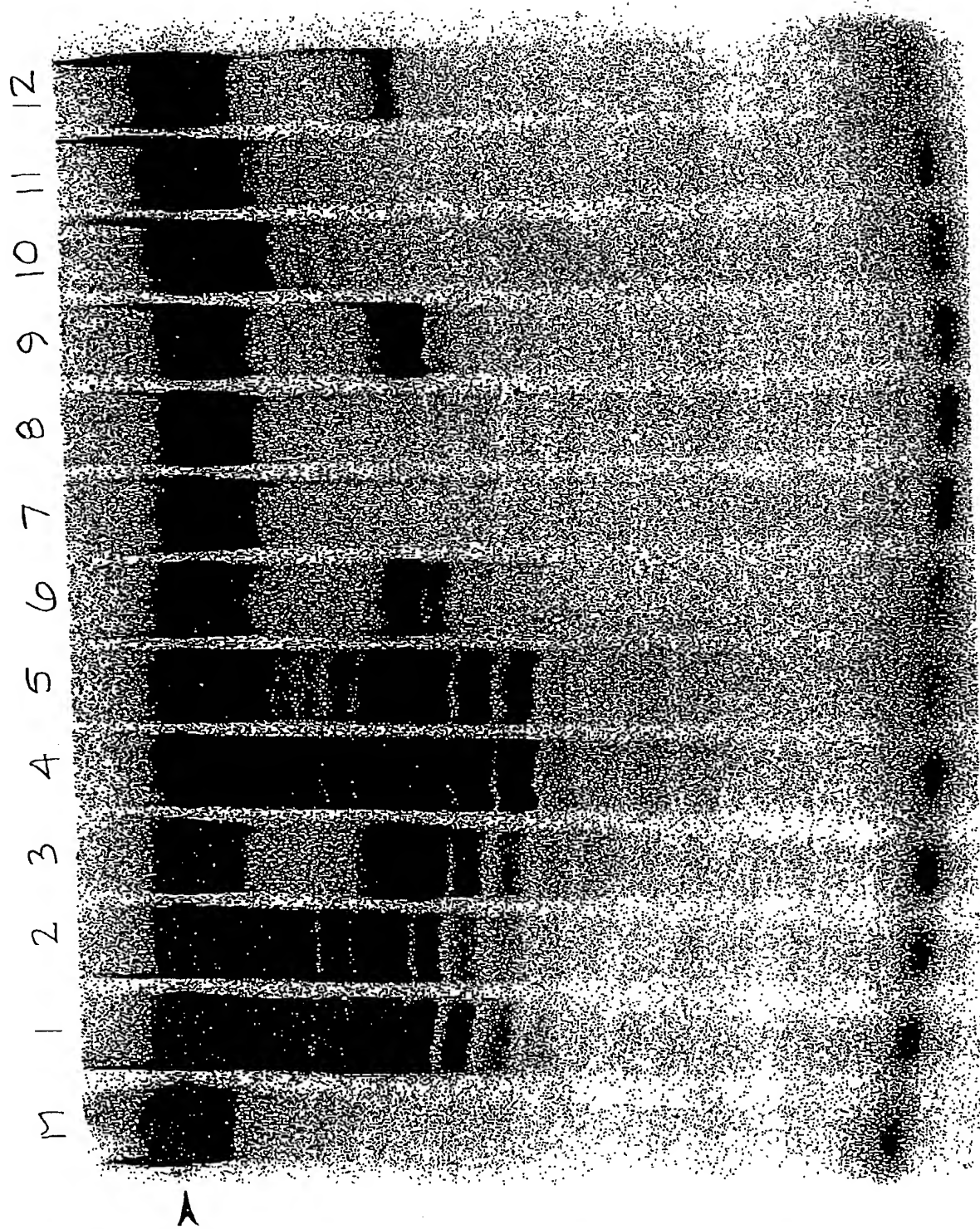
2

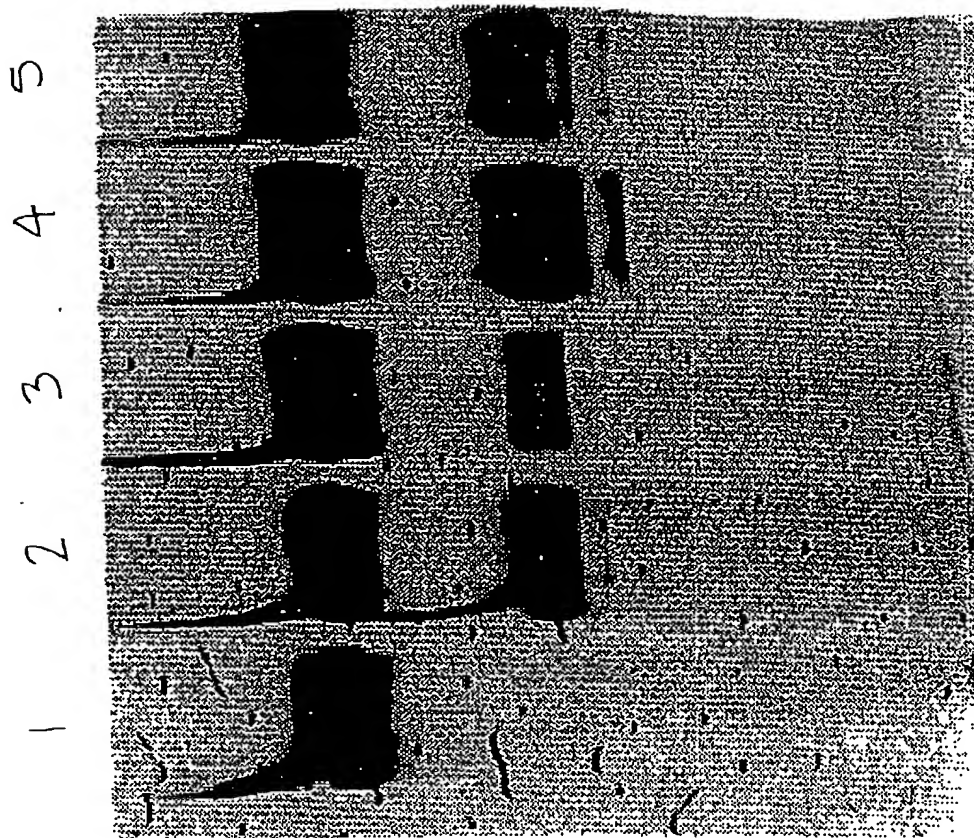
Abstract

A 2

45

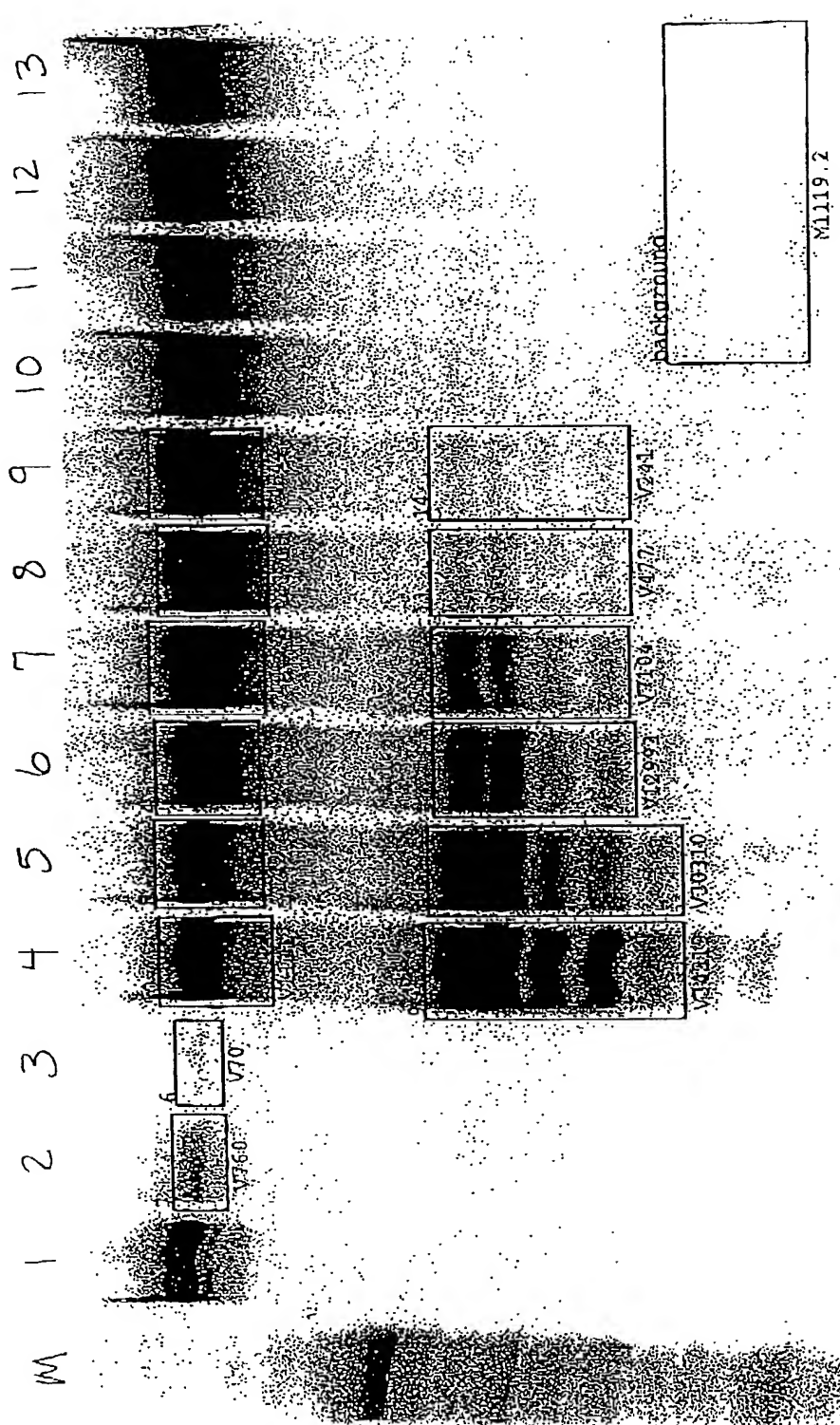
FIGURE 34



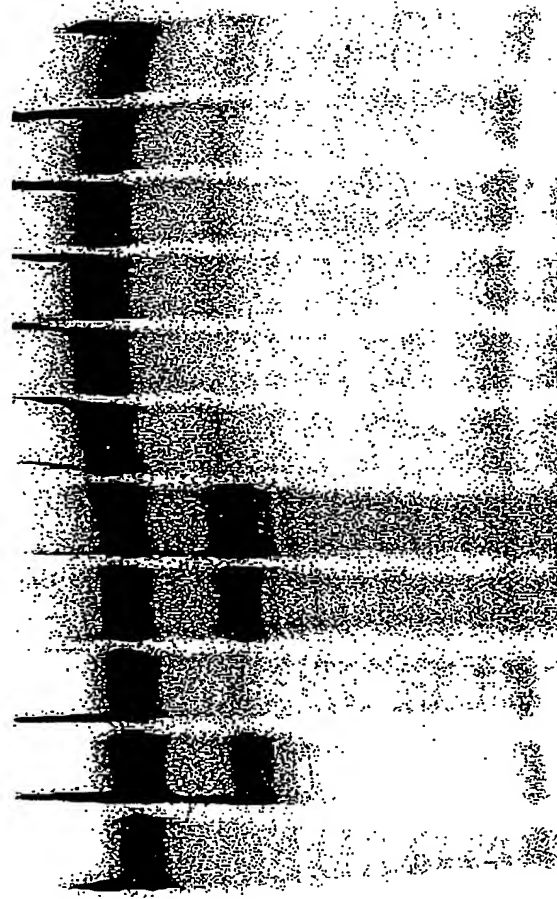


26

FIGURE 36



1
2
3
4
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10
11



A A

FIGURE 38

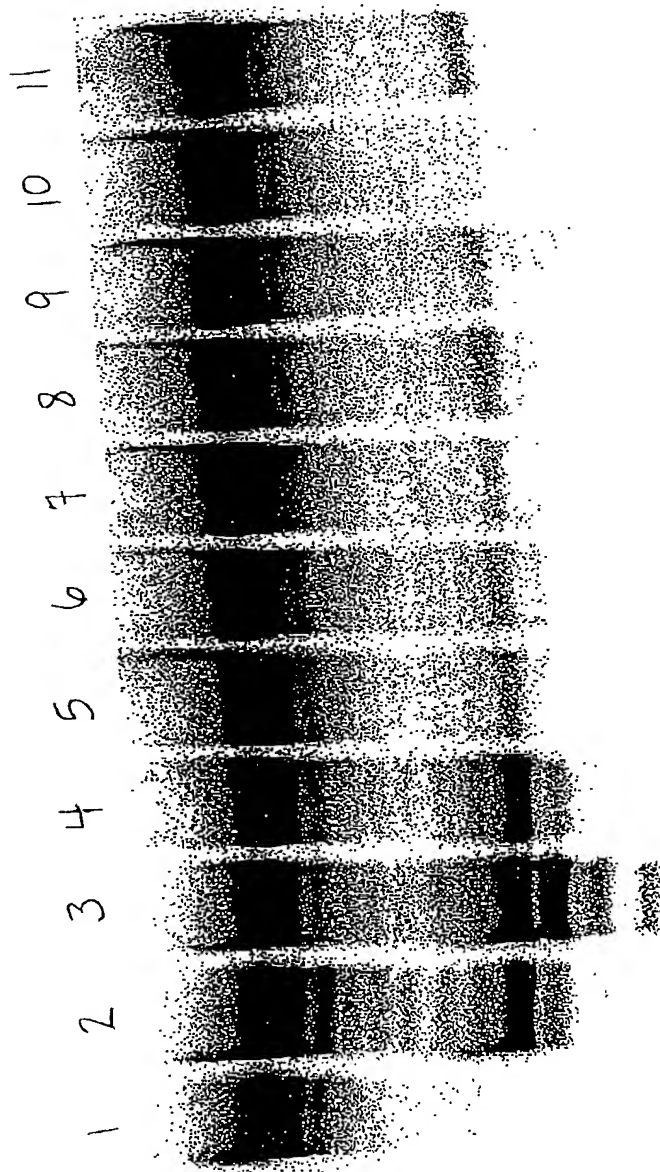


FIGURE 39

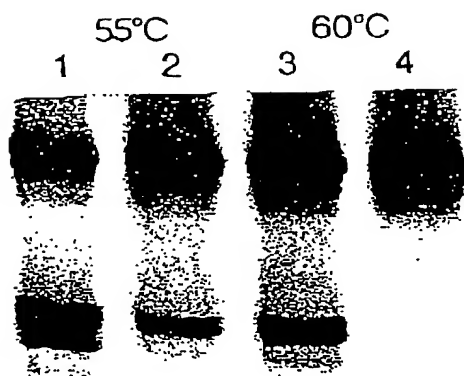


FIGURE 40

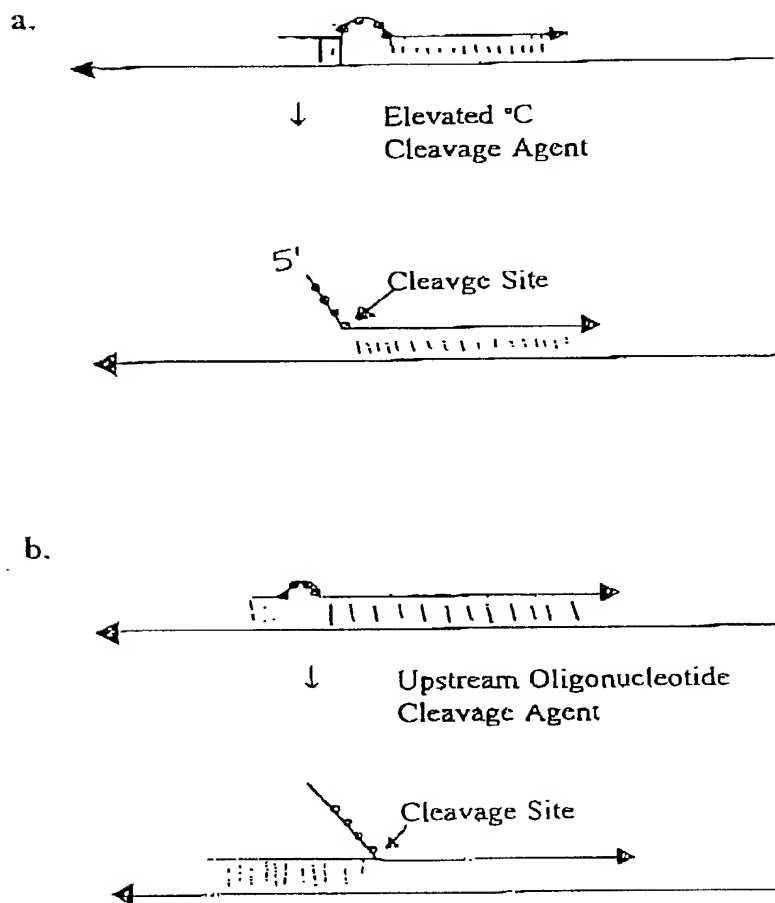


FIGURE 41

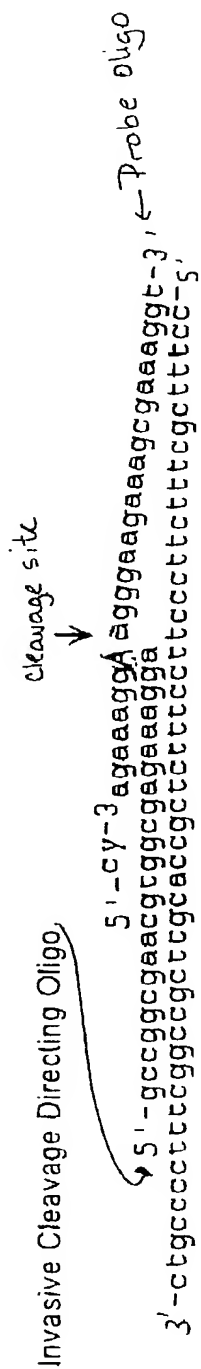


FIGURE 42

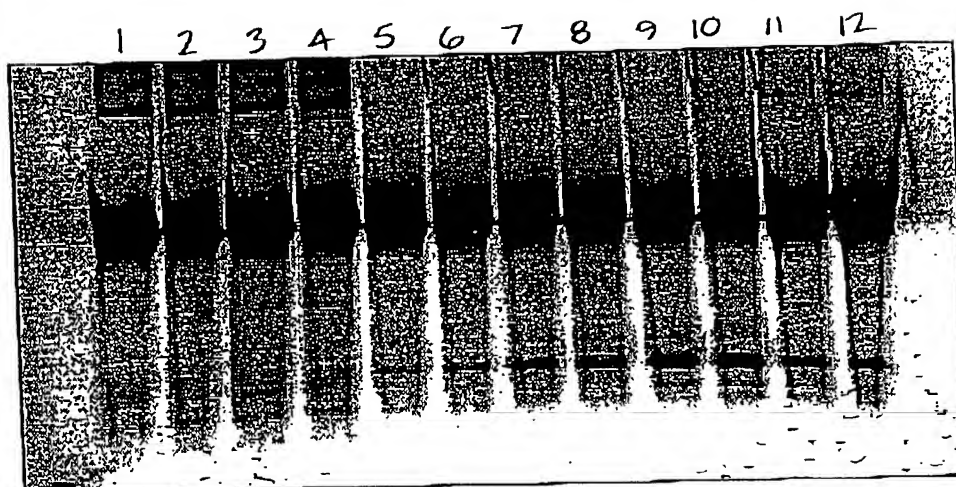


FIGURE 43

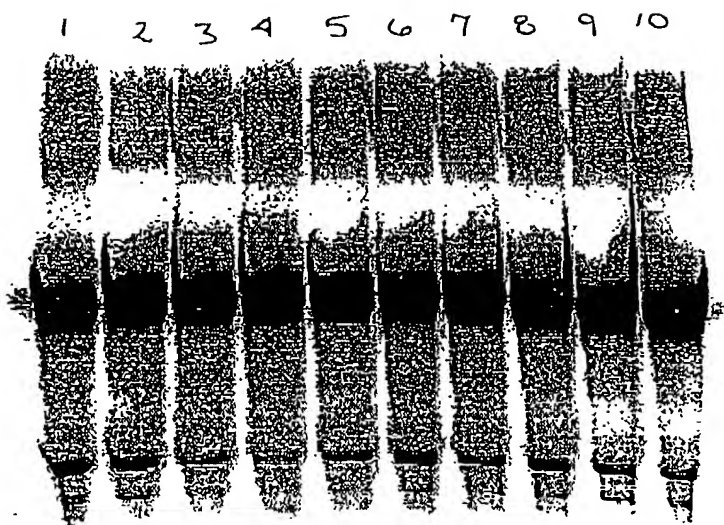


FIGURE 44

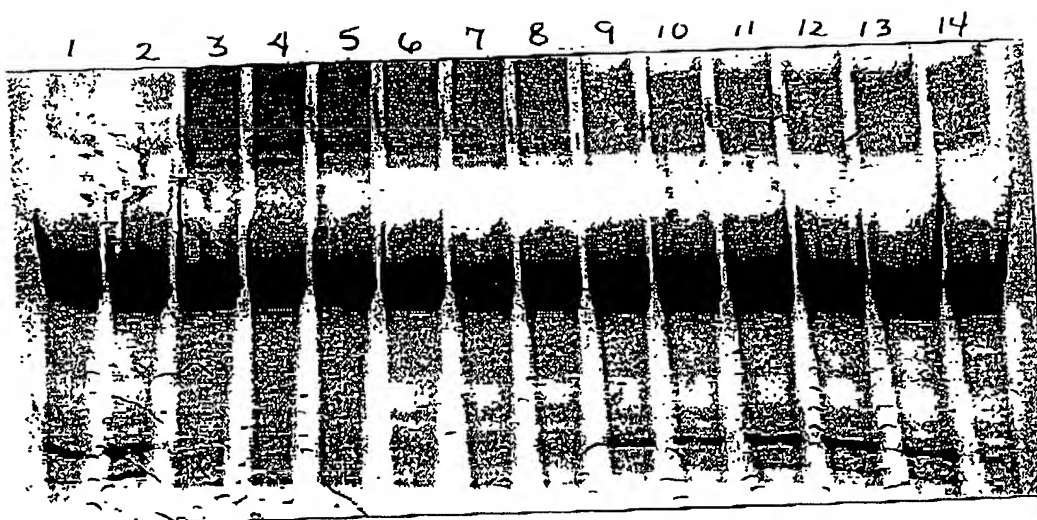


FIGURE 45

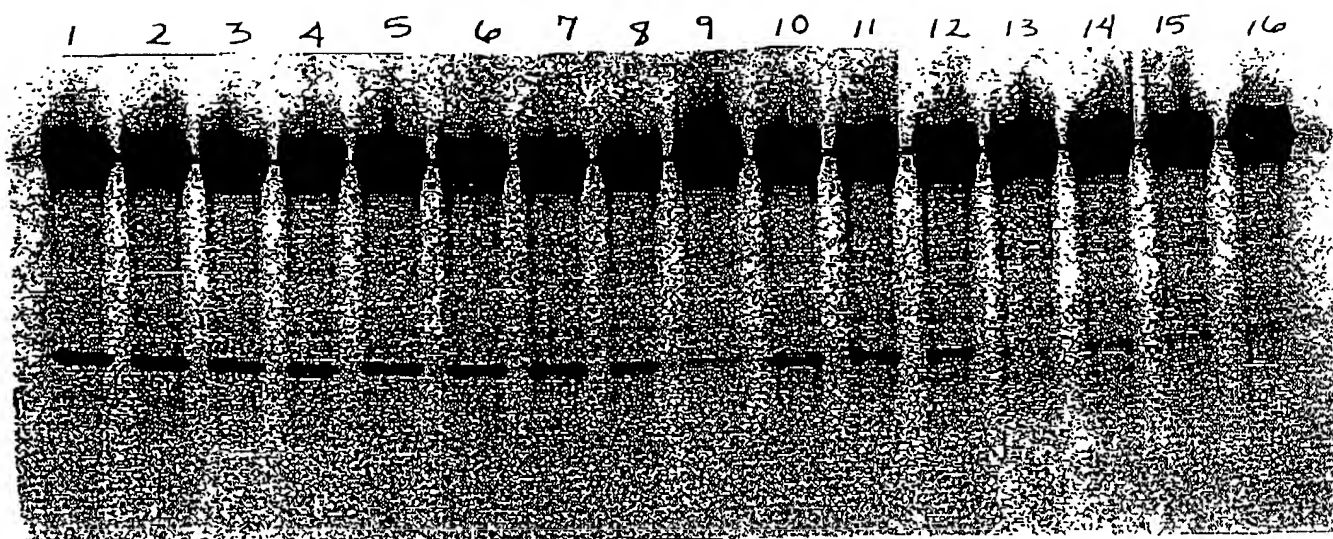


FIGURE 46

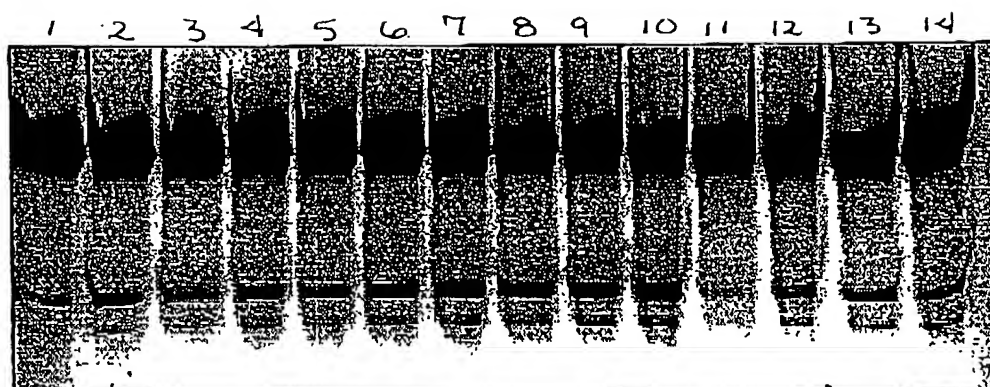


FIGURE 47

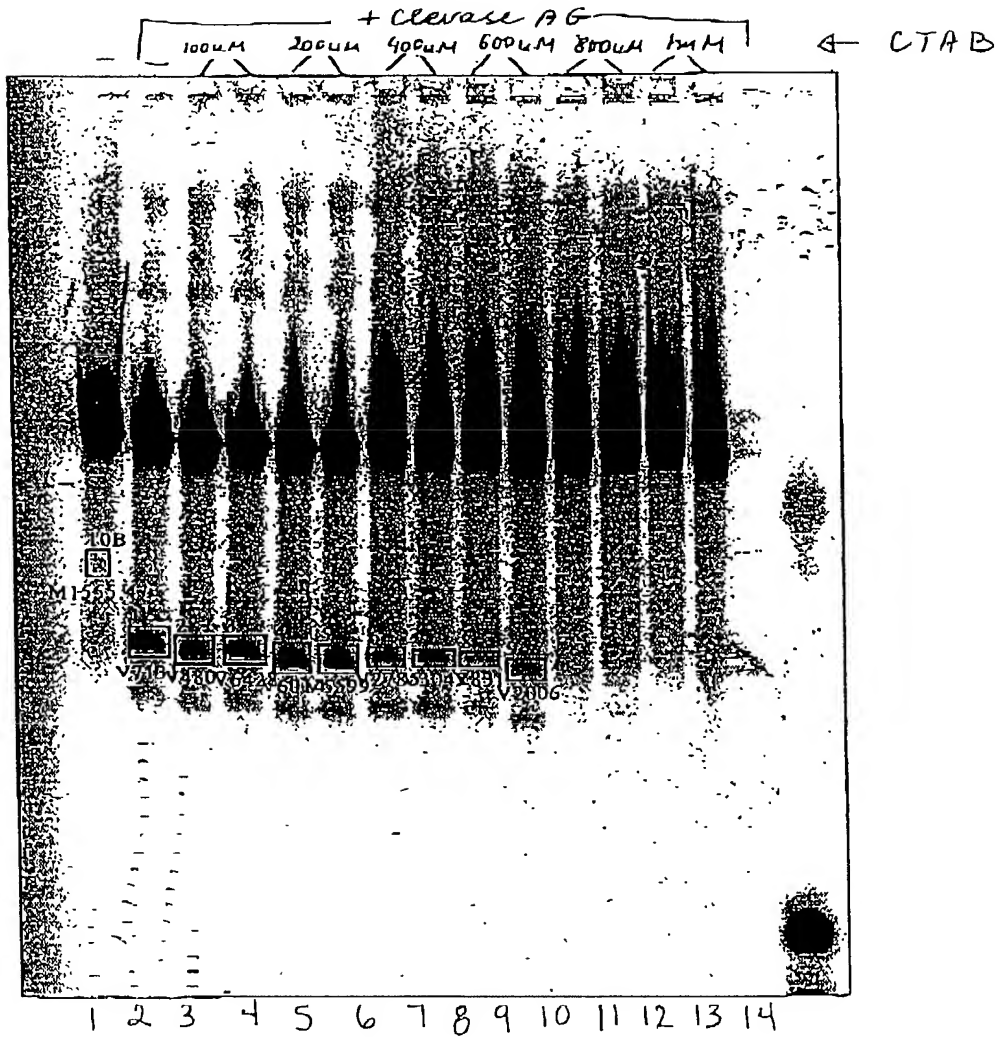


FIGURE 48

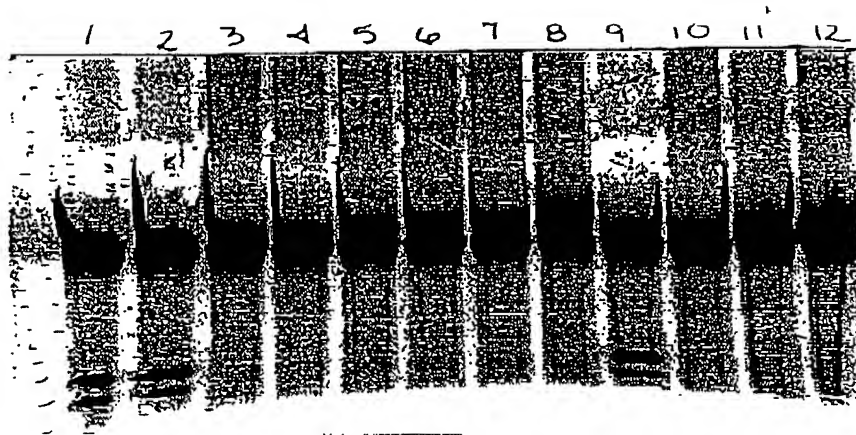


FIGURE 49

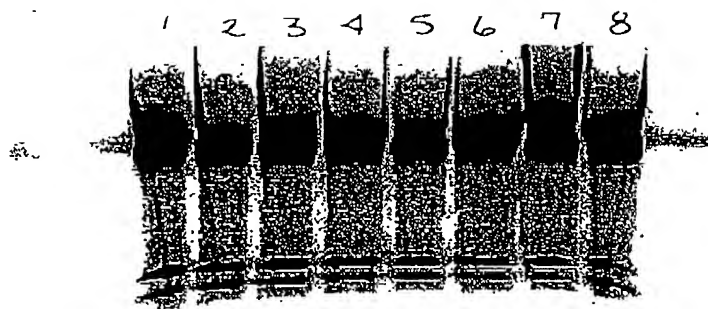


FIGURE 50

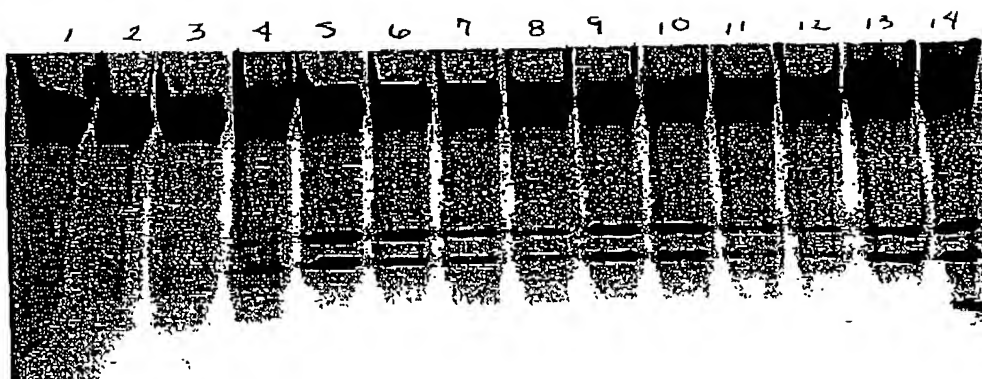


FIGURE 51

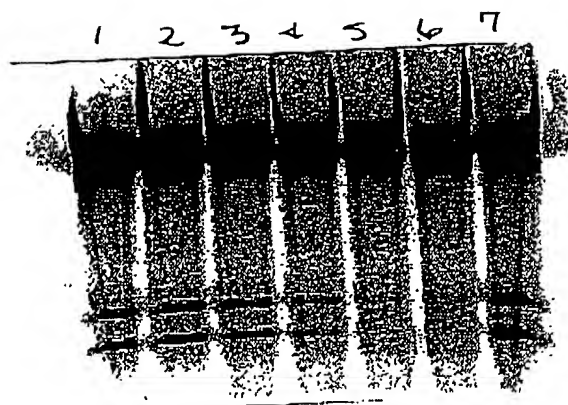


FIGURE 52

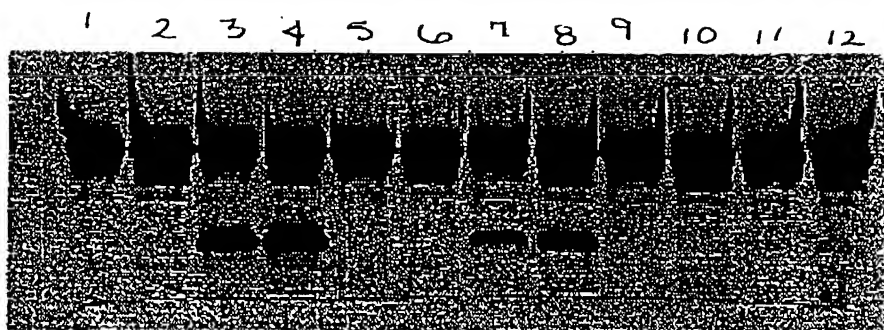


FIGURE 53

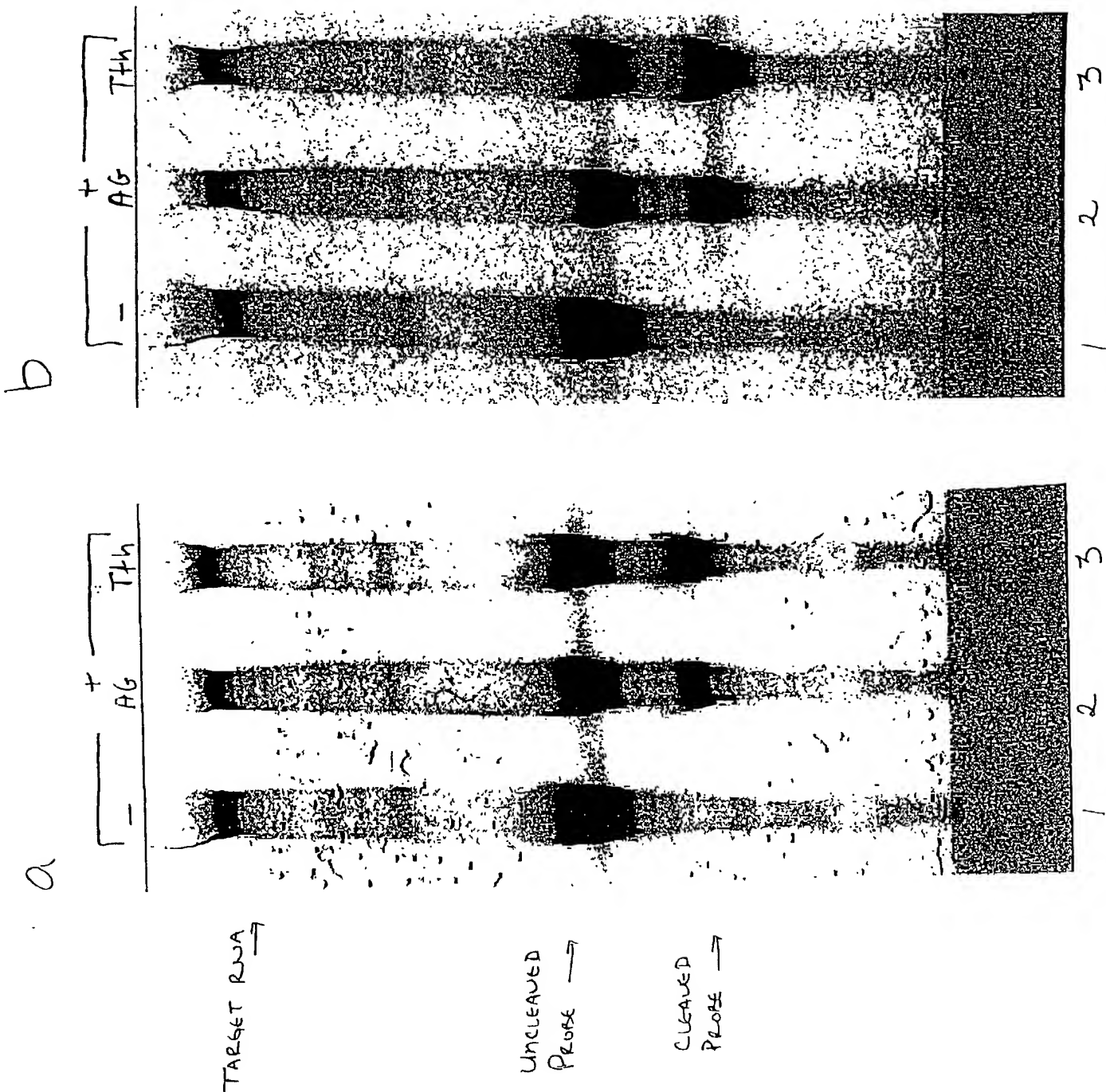


FIGURE 54

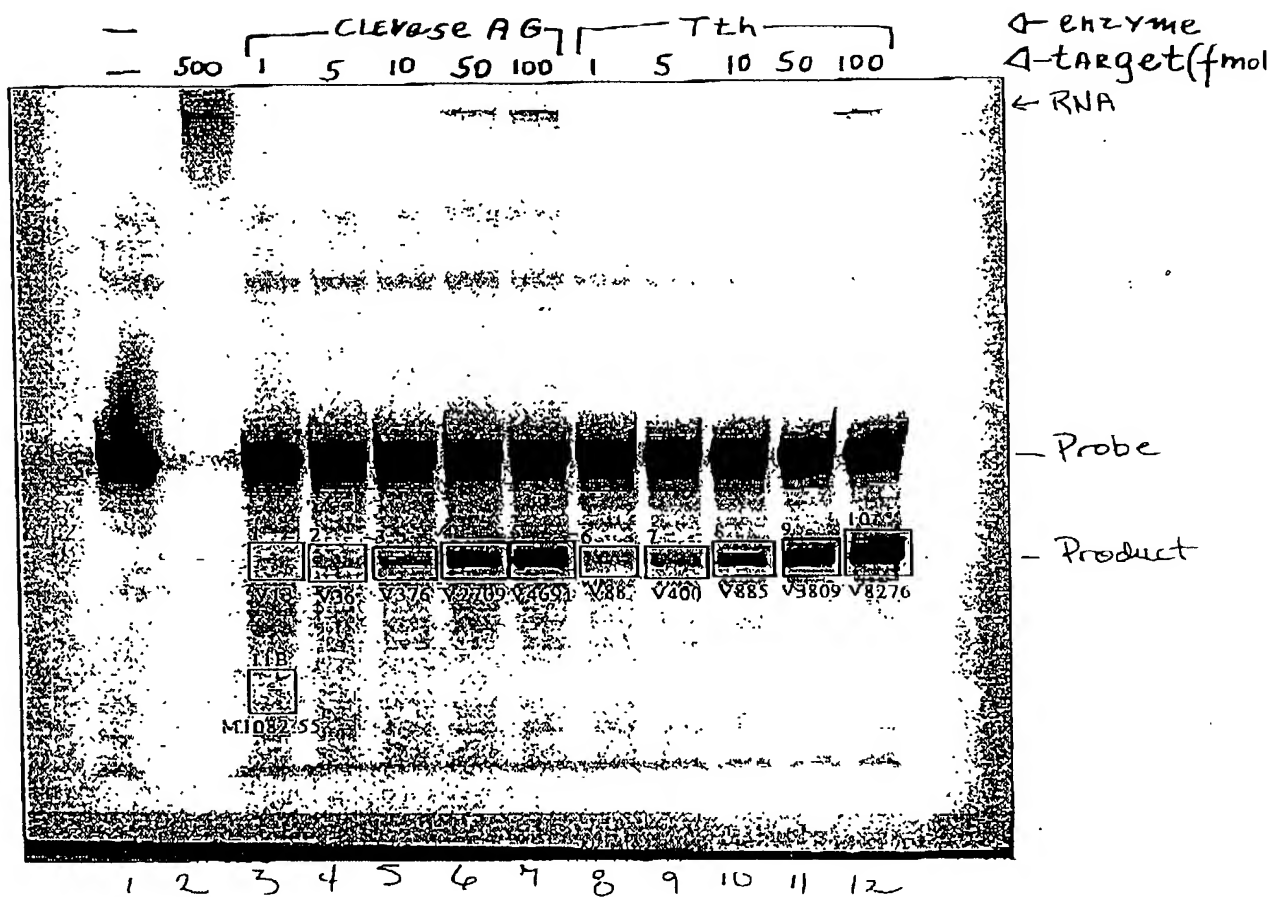


FIGURE 55

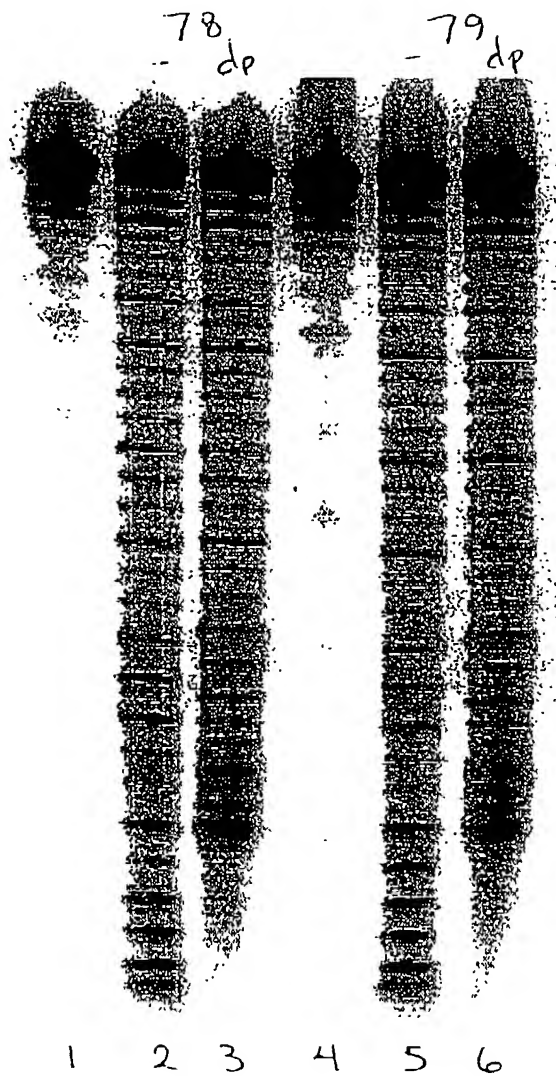


FIGURE 56

70 (C10 aminoT's)

74 (C6 amino T's)

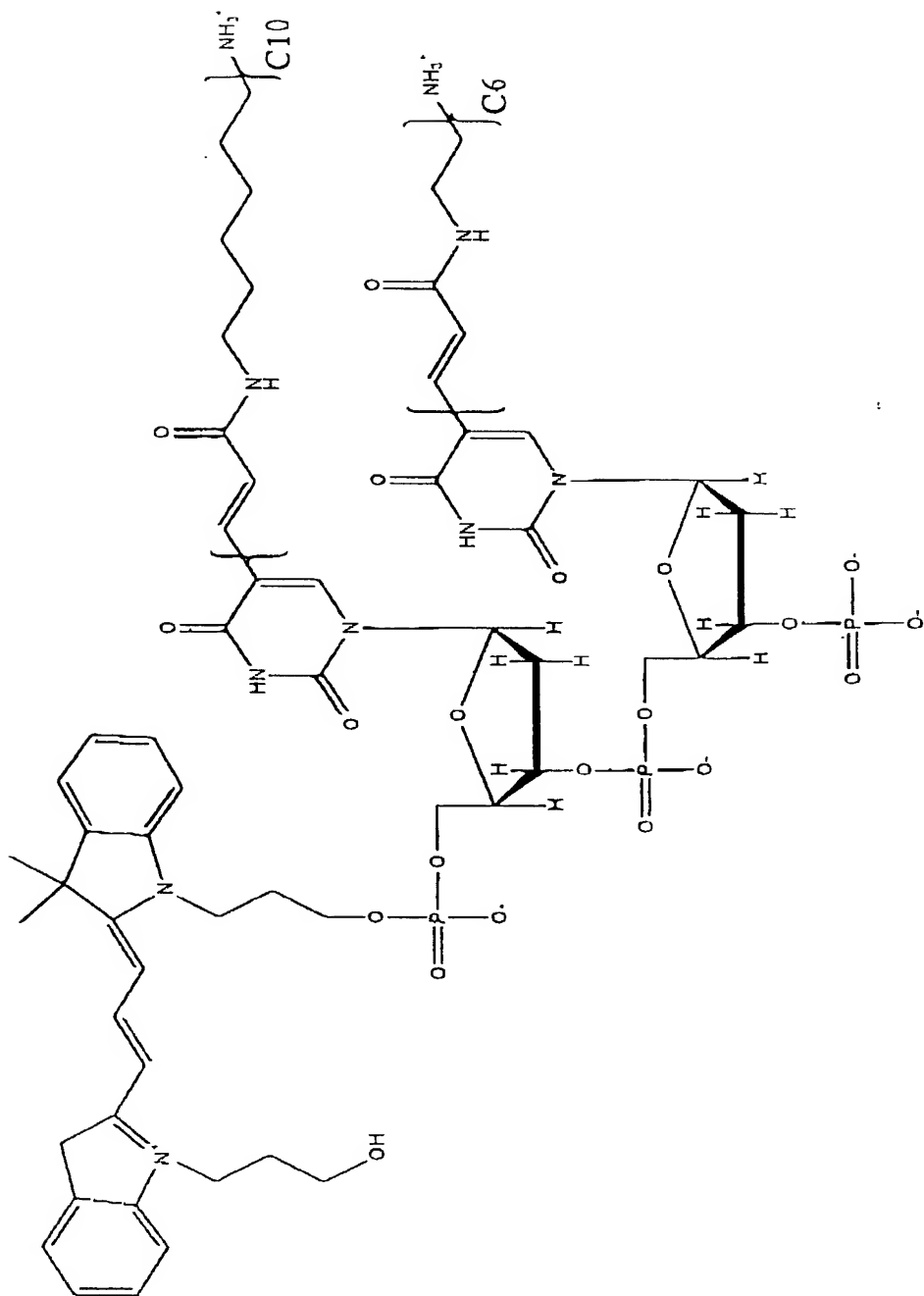


FIGURE 57

75

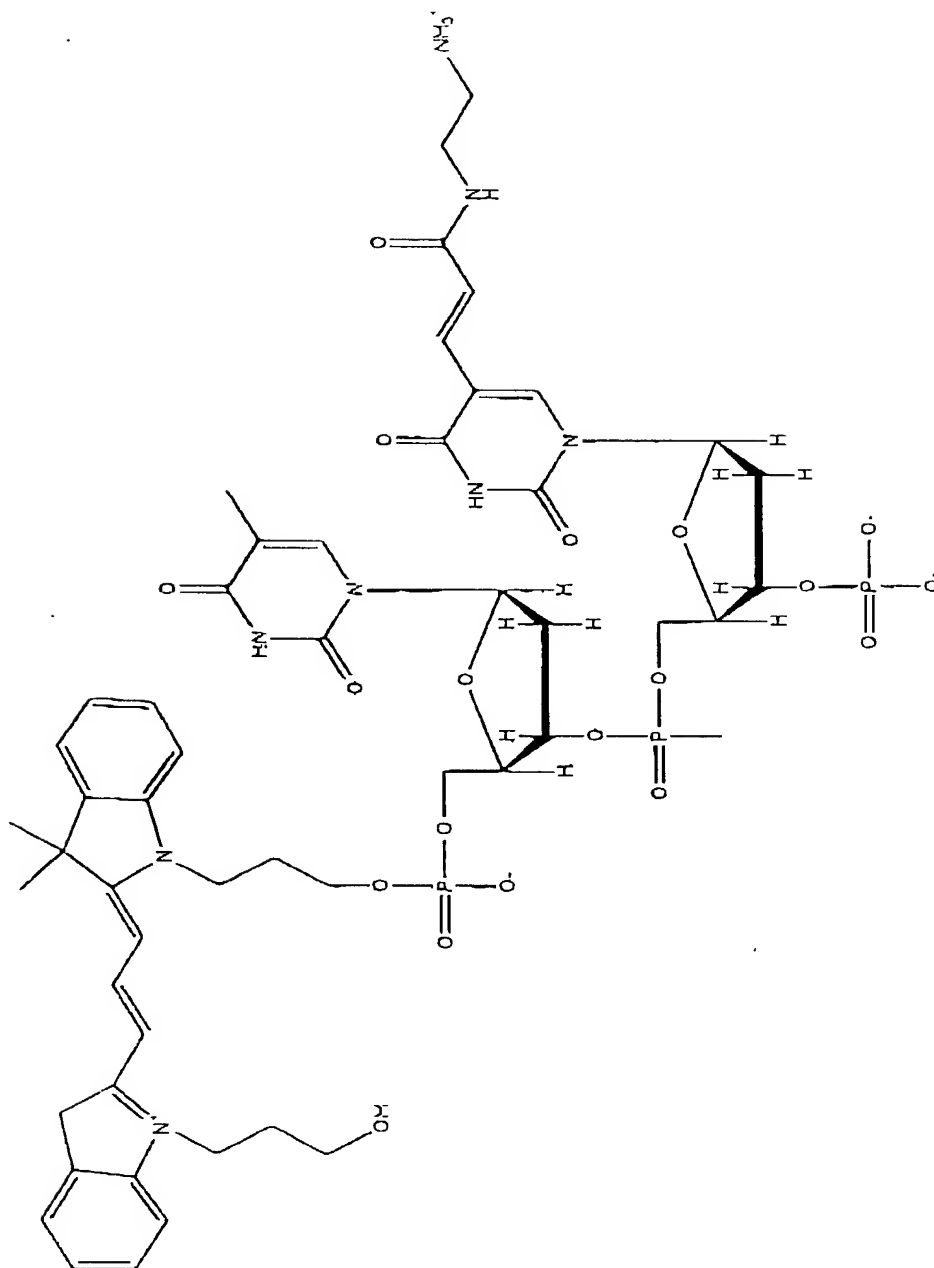
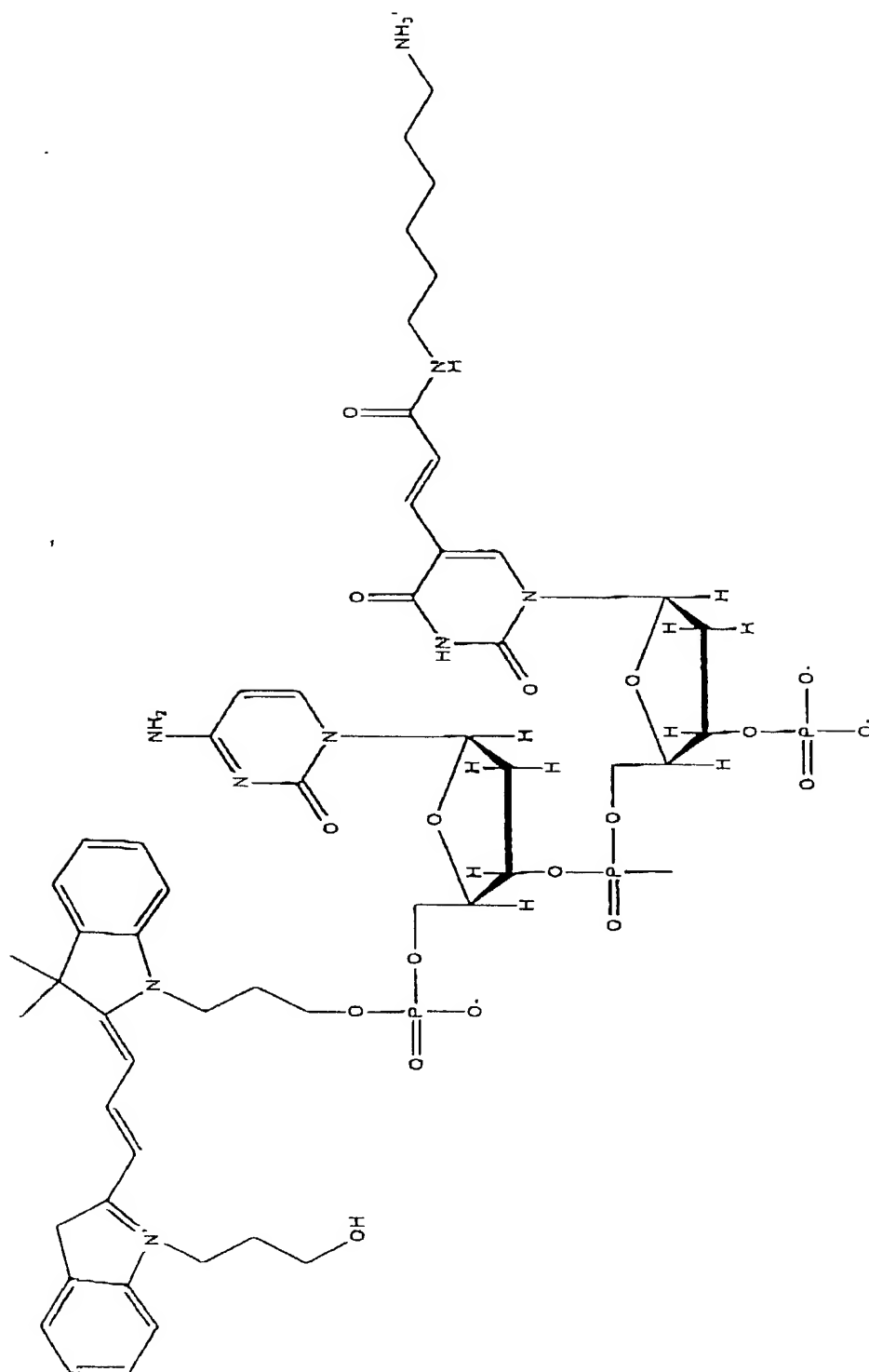


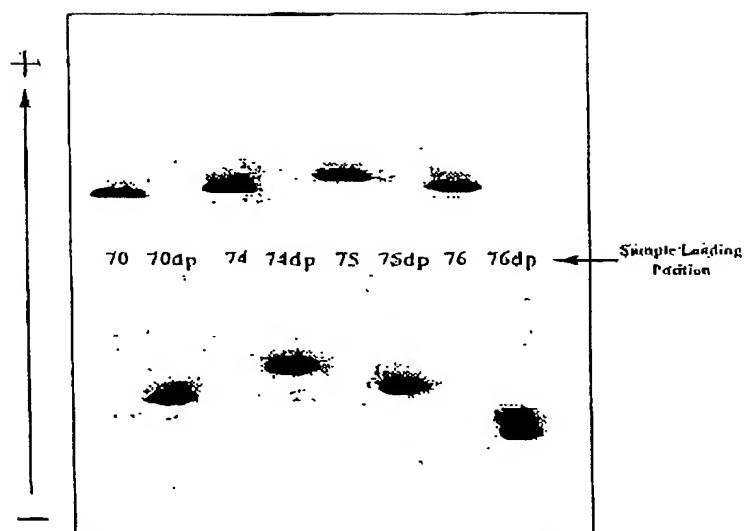
FIGURE 58



76

70

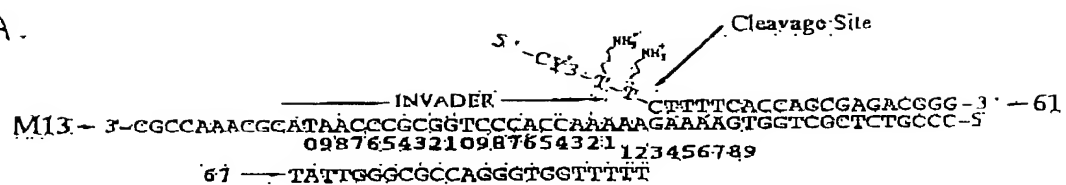
FIGURE 59



71

FIGURE 60

A.



B.

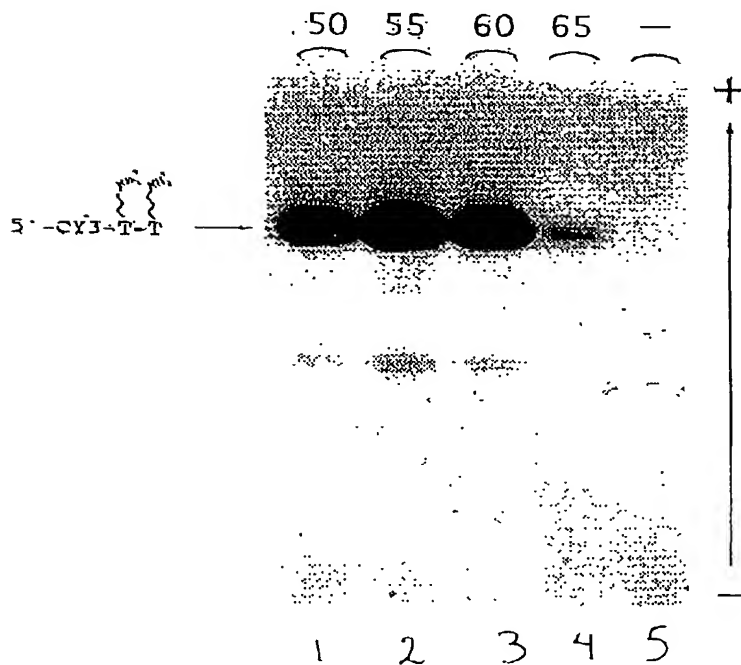


FIGURE 61

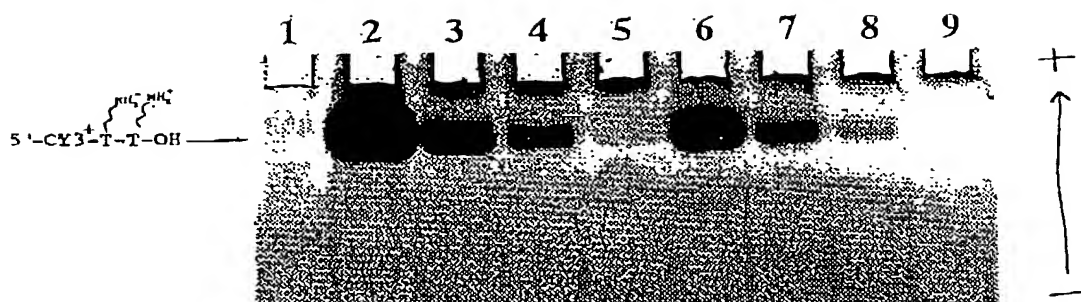
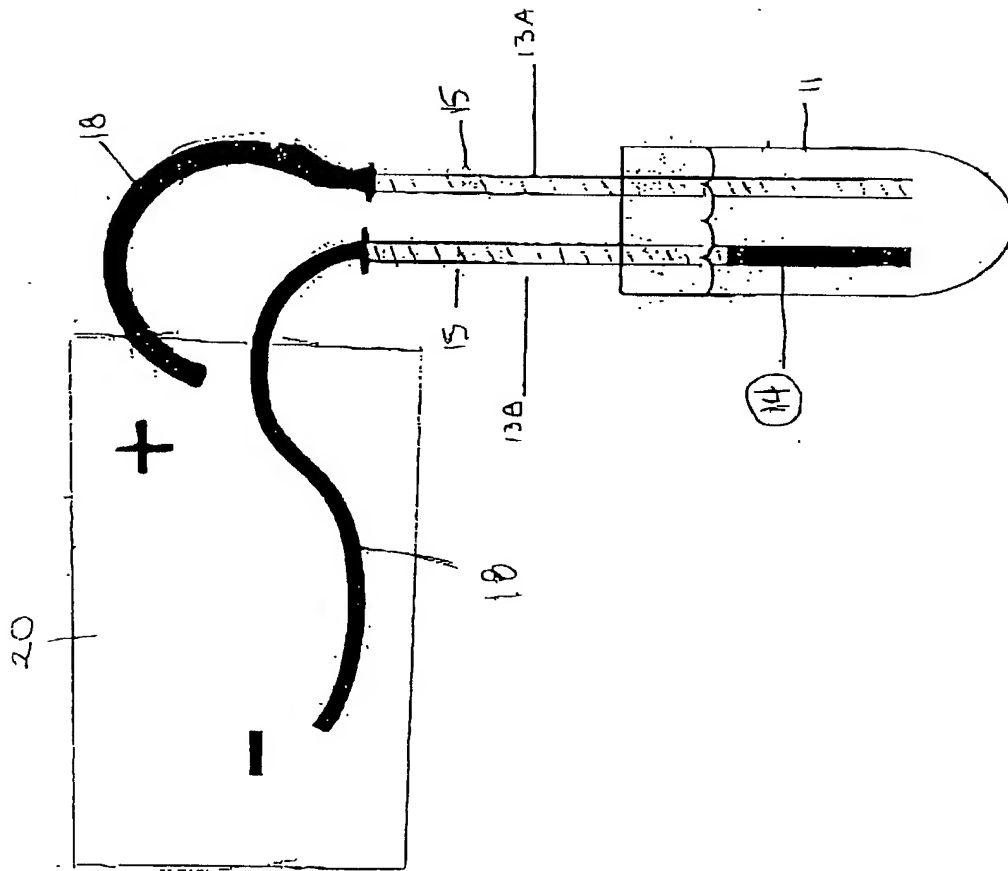


FIGURE 62



74.

FIGURE 63

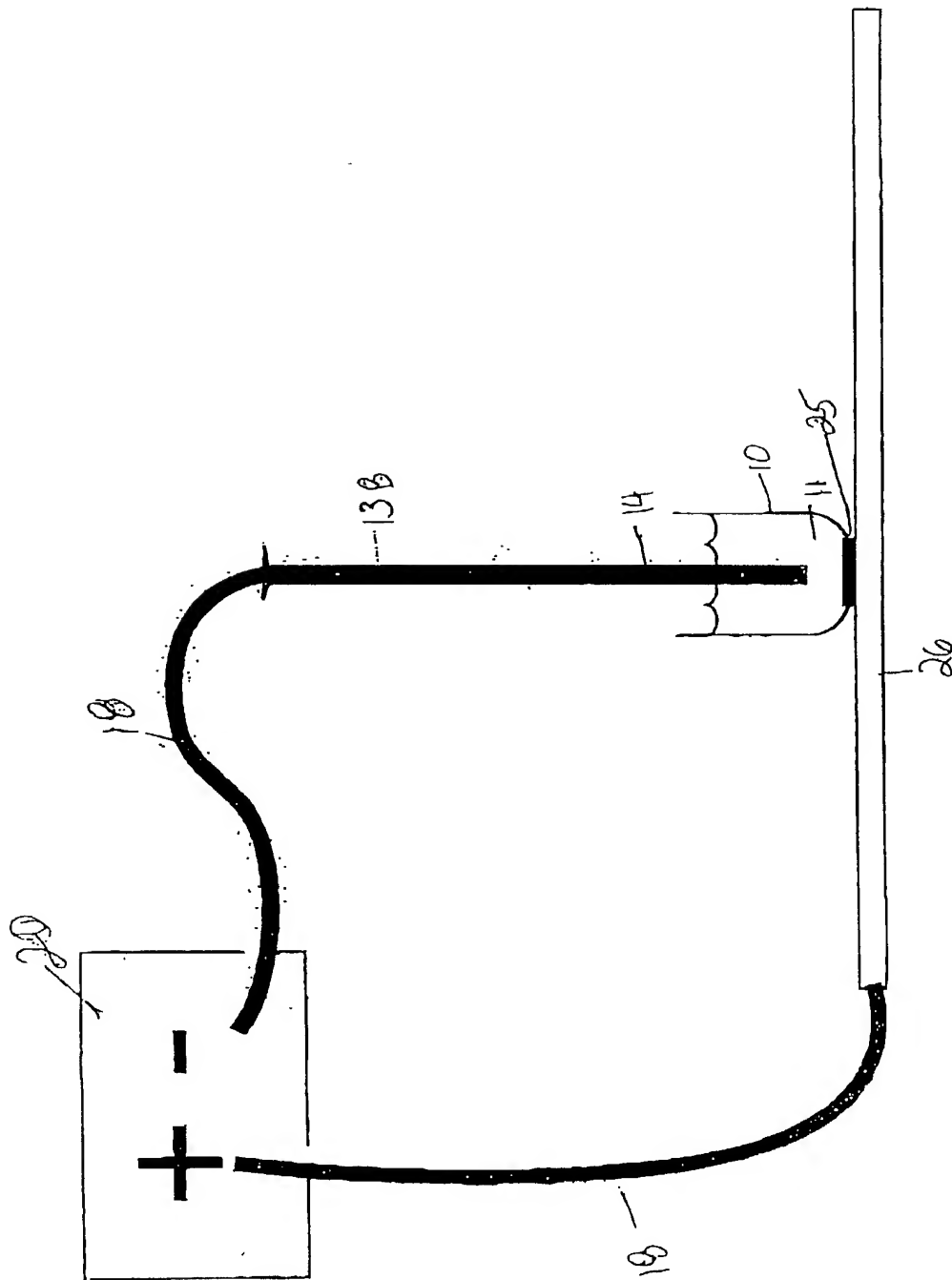


FIGURE 64

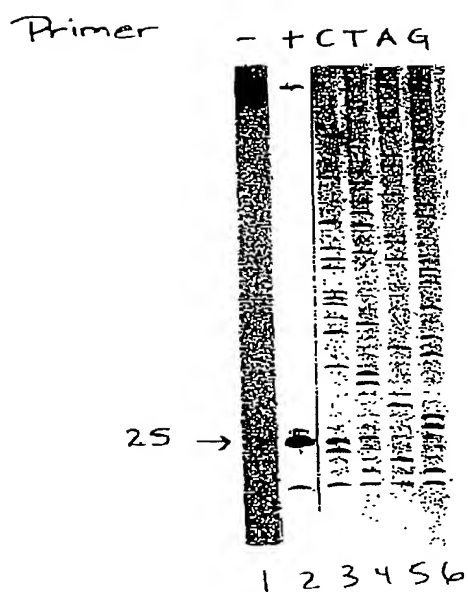


FIGURE 65

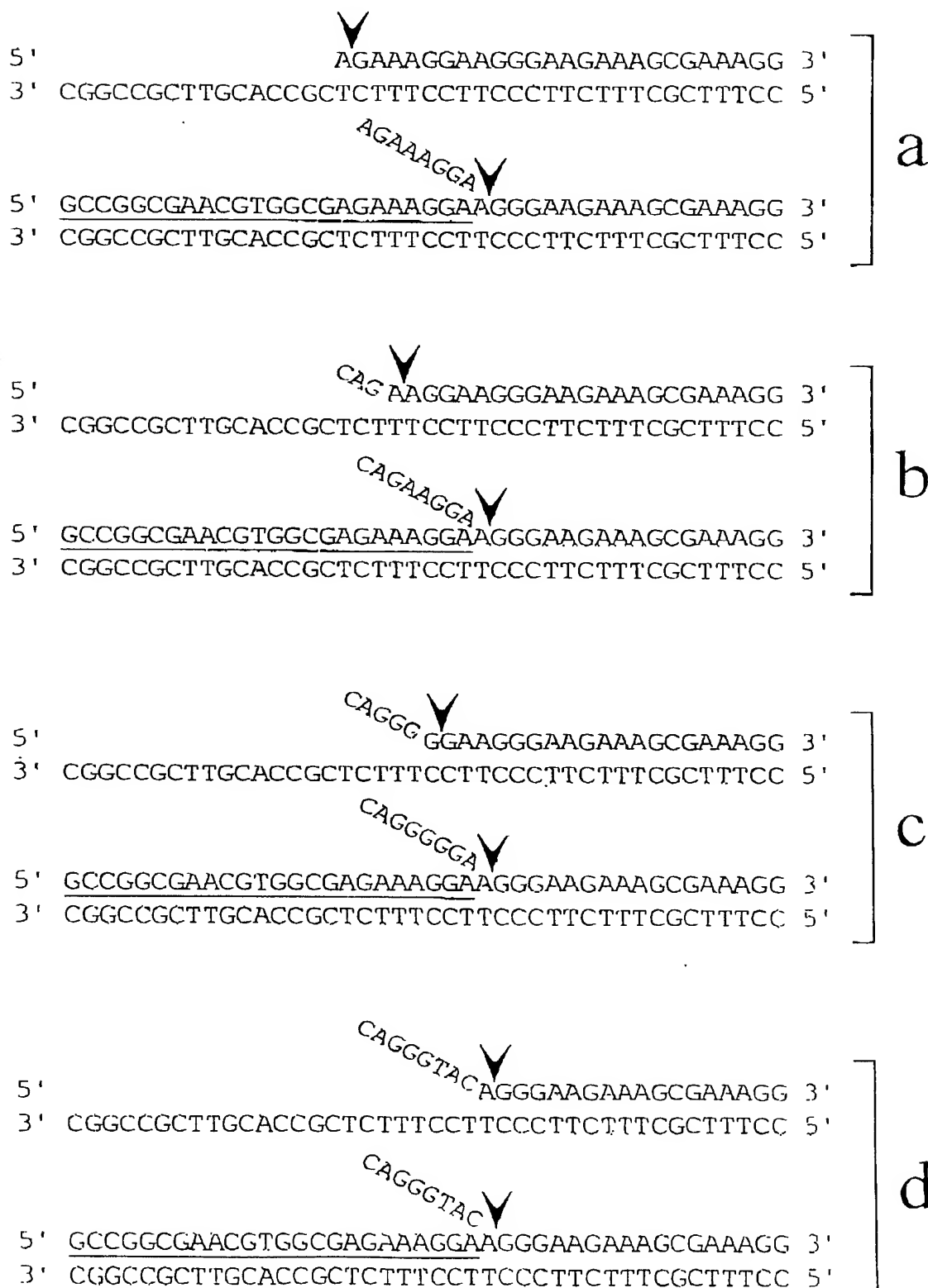


FIGURE 66

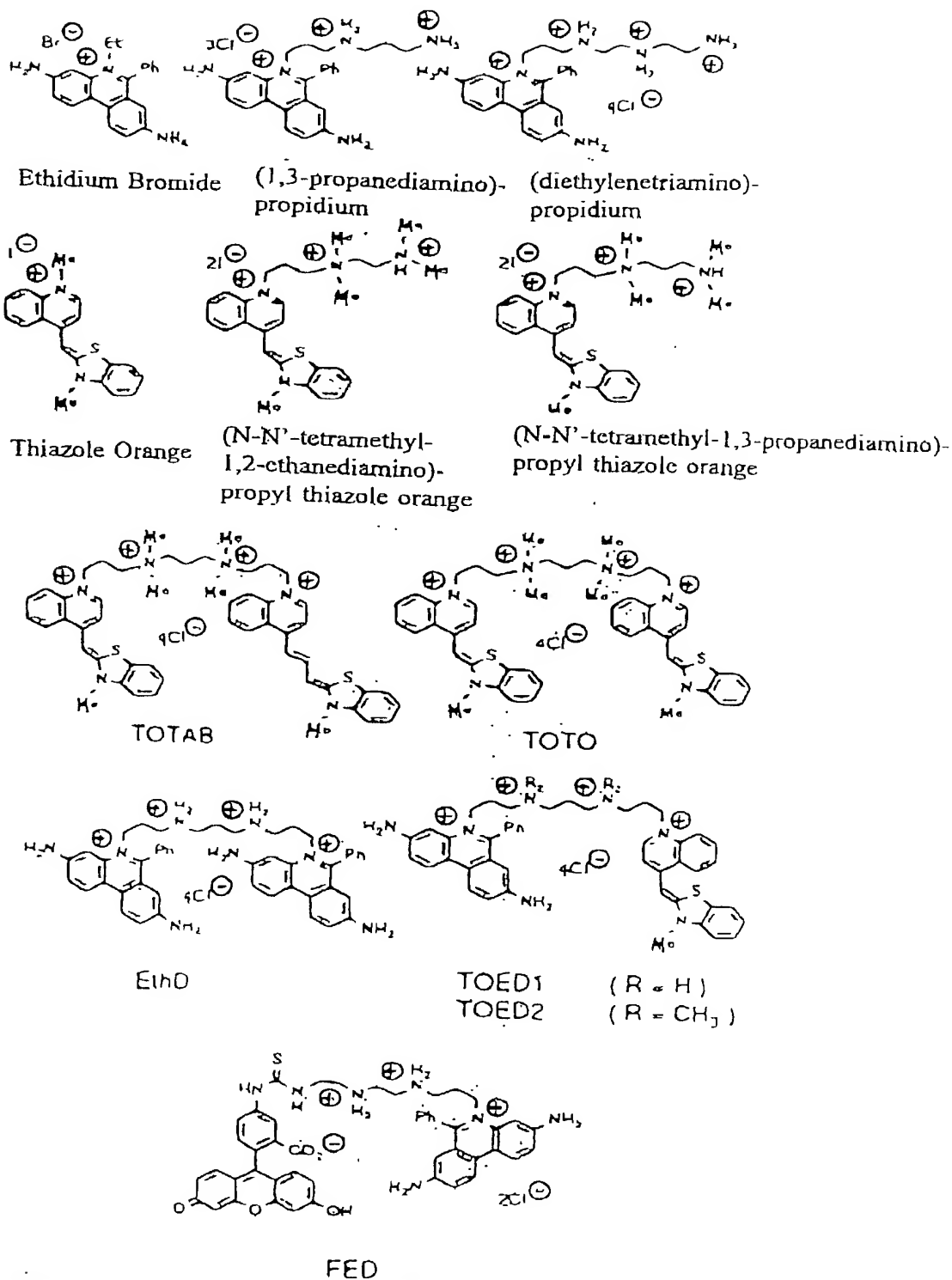


FIGURE 67

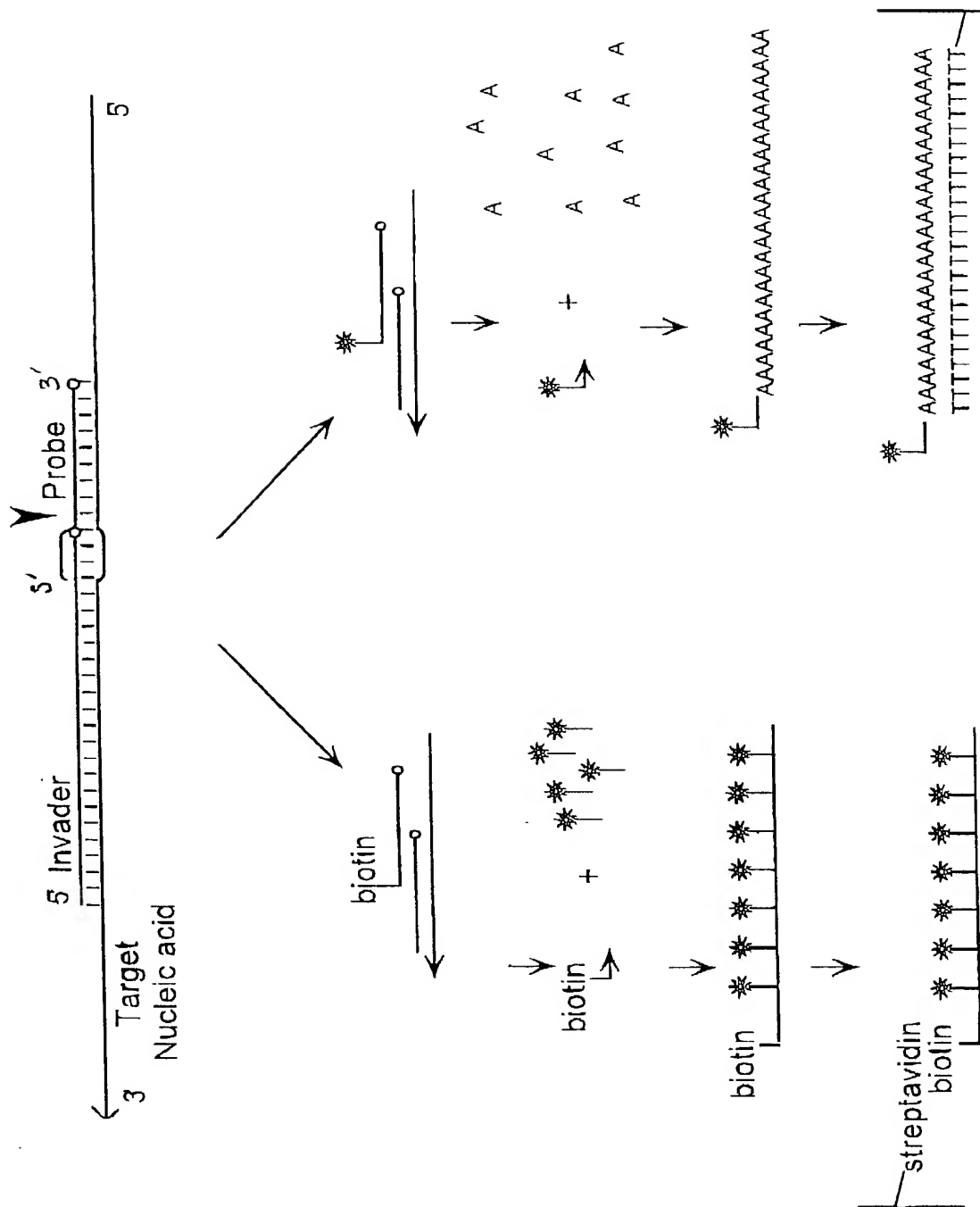


FIGURE 68

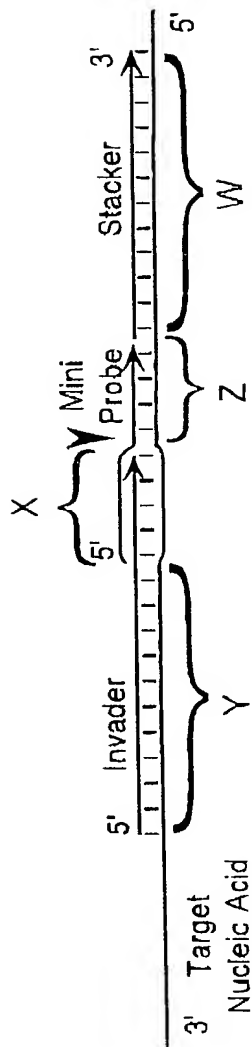


FIGURE 69

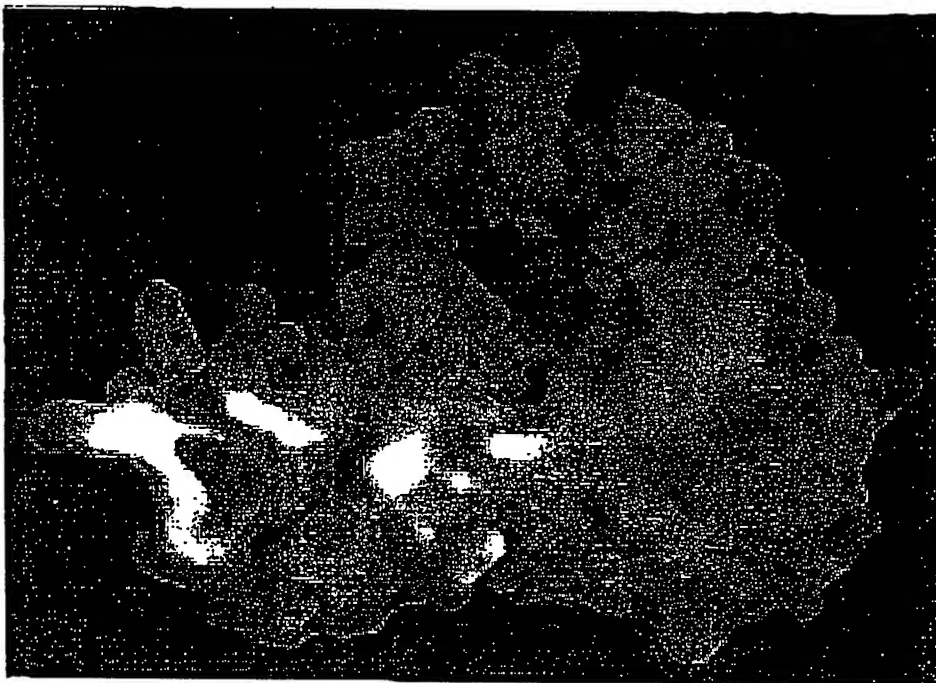


FIGURE 70-A

	10	20	30	40	50	60	70							
MGVO	-----	FGDF	IPK--NI	ISFEDL	KGKKVA	IDGMNAL	YQFLT	SIRLRD	GSPLRNR	KGEJ	TSAYNG	VFY	MJAFEN	1.PRO
MGVP	-----	IGEJ	IPR--	KEIELEN	LYGKK	IAIDALNA	IYQFLT	STIROK	DGTPLMD	SKGR	ITSHLS	GLFY	PFUFEN	1.PRO
MGIO	QGLAKL	IADVAPSA	IENDIKSY	FGRKVA	IDASMS	IYQFL	IAVRO	GGDVL	QNEEGE	TTSHLM	GMFY		HUMFEN	1.PRO
MGIH	GLAKL	IADVAPSA	IENDIKSY	FGRKVA	IDASMS	IYQFL	IAVRO	GGDVL	QNEEGE	TTSL	LMGMFY		MUSFEN	1.PRO
MGIK	GLNAT	ISEHVPSA	IRKSDIK	SFFGRKVA	IDASMS	IYQFL	IAVRO	DDGGQL	TNEAGET	TTSHLM	GMFY		YST510	1.PRO
MGVH	SFWD	IAG----	PTARPVR	LESLED	KRMAYD	ASIW	IYQFL	KAVRDO	EGNAVKN	-----	SHITG	FFR	YSTRAD2	1.PRO
MGVS	GLWNLE	----	PVKRPV	KLET	LVNKR	LADASI	W	IYQFL	KAVRDK	EGNOLKS	-----	SHVVG	SPORAD13	1.PRO
MGVO	GLWKLE	----	CSGRQV	SPEALE	GK	ILAVD	ISWL	NOALK	GVDRDR	HGNS	IEN-----	PHLL	TLFH	HUMXPG
MGVO	GLWKLE	----	CSGHRV	SPEALE	GK	VLAVD	ISWL	NOALK	GVDRSH	GNV	IEN-----	AHLL	TLFH	MUSXPG
MGVO	GLWKLE	----	CSGRP	INPGT	LEGK	ILAVD	ISWL	NOAVK	GARDRO	GN	AIEN-----	AHLL	TLFH	XENXPG
MTING	IWEWANH	VV----	RKVPNET	MRK	TL	SIDGHI	WL	YESL	KGCEAH	HQOT	-----	PNSYL	VTF	CELRAD2

[illegible]

FIGURE 70-B

	150	160	170	180	190	200	210
130	KMVENCKYLLSLMGIPYVEAPSEGEAQAASMAKKGQVAVVSQDYDALLYGAPRVVRNLT	TTTKEM----					MJAFEN1.PRO
130	MLJEDAKKLELMGIPYVOAPSEGEAQAAYMAAKGSVYASASQDYDOLLLFGAPRLVRNLT	ITGKRKLPGK					PFUFEN1.PRO
136	QHNOECKHLLSLMGIPYLDAPSEAEASCAALVKAGKYAAATEMDCLTFGSPVLMRHLT	ASEAKKLPJO					HUMFEN1.PRO
134	QHNOECKHLLSLMGIPYLDAPSEAEASCAALAKAGKYAAATEMDCLTFGSPVLMRHLT	ASEAKKLPJO					MUSFEN1.PRO
134	EHNEEAQKLLGLMGIPYIJAPEAEAOCAELAKKGKYAAASEMDTLCYRTPFLLRHLT	TFSEAKKEPIH					YST510.PRO
131	OMIKEVOELLSRFGIPYITAPMEAEAOCAELLOLNLVDGIITDDSOVFLFGGTRVYRNMF	NONKF----					YSTRAD2.PRO
131	YMIKECOELLRLFGLPYIYAPQEAEOCAELKLEKLVGIVTDDSDVFLFGGTRVYRNMF	NONKF----					SPORAD13.PRO
131	OMFLESQELLRLFGLPYIYAPQEAEOCAELKLEKLVGIVTDDSDVFLFGGTRVYRNMF	NONKF----					HUMXPG.PRO
131	OMFLESQELLRLFGLPYIYAPQEAEOCAELKLEKLVGIVTDDSDVFLFGGTRVYRNMF	NONKF----					MUSXPG.PRO
131	OMCLESQELLRLFGLPYIYAPQEAEOCAELKLEKLVGIVTDDSDVFLFGGTRVYRNMF	NONKF----					XENXPG.PRO
111	DHVKYTNALLTELGIKYIAPGQEAOCARLEDLGVTSGCITTDFOYFLGGKNLYRFD	TAGT-----					CELRA22.PRO

	220	230	240	250	260	270	280
195	-----PELIELNEVLEDLRISLDDLIDJAFMGTDYNPGGV--K--GIGFKRAYELVRSGVAK--DV						MJAFEN1.PRO
200	NVYVE-1KPELILEEVVKELKLTREKLIELAILVGTDYNPGGI--K--GIGLKKALEIVRHSKDPLAKF						PFUFEN1.PRO
206	EFHLSRILDELGLNOEQFVLCILLGSDYCESIRGIGPKRAVDLIQK--HKSIEEIVRRLOPN----						HUMFEN1.PRO
204	EFHLSRVLOELGLNOEQFVLCILLGSDYCESIRGIGAKRAVDLIQK--HKSIEEIVRRLOPN----						MUSFEN1.PRO
204	EIDTELVRGLDLTIEQFVLCILLGSDYCESIRGIGPKRAVDLIQK--HKSIEEIVRRLOPN----						YST510.PRO
198	FYDAESILKLLGLDRKNMIELAQLLGSQDYTNGLKGMGPVSSIEVIAEF--GNLKNFKDWYNNGOFOK						YSTRAD2.PRO
198	LYLMODMKREFNVNOMDLIKLAHLLGSQDYTNGLSRVGPVLALEILHEFPDGTGLFEKKWFQRLSTGHAS						SPORAD13.PRO
198	YYQYVDFHNLGLDRNKLINLAYLLGSQDYTEGIPTVGCVTAMEILNEFPGRGLDPLKFSWHEAQNK						HUMXPG.PRO
198	YYQYVDFYHNLGLDRNKLINLAYLLGSQDYTEGIPTVGCVTAMEILNEFPGRGLDPLKFSWHEAQNK						MUSXPG.PRO
198	YYQYADFHNLGLDRSKLINLAYLLGSQDYTEGIPTVGYVSAMEILNEFPGRGLDPLKFSWHEAQNK						XENXPG.PRO
175	-----SSTACLDHIMHLSLGRMF-----						CELRA22.PRO

FIGURE 70-C

	290	300	310	320	330	340	350	
251	LKKEVEYYDEIKRIFKEPKV----	-----	-----	-----	TO--NYSLSLKLDPDKEGI	KFLVDOENDFNVD	MJAFEN1.PRO	
265	QKOSDVOLYAIKEFFLNPPV----	-----	-----	-----	TD--NYNLVWROPOEEGIL	KFLCOEHDFSEE	PFUFEN1.PRO	
269	PVPENWLHKEAHQLFLEPEV----	-----	-----	-----	LPESVELKWSEPNEEEEEL	KFMCGEKFSEE	HUMFEN1.PRO	
267	PVPENWLHKEAQOLFLEPEV----	-----	-----	-----	VOPESVELKWSEPNEEEEEL	VKFMCGEKFSEE	MUSFEN1.PRO	
272	KIPEDWPYKQARMLFLDPEV----	-----	-----	-----	IDGNEINLKWSPPKEKEL	I EYL COOKKFSEE	YST510.PRO	
265	QETENKFEKDRLKKLVNNEI	(LODDFPSVMVYDAYMRPEVD	HTT	PFVVGVPOLM	LSFMTOLGWPH	E	YSTRAD2.PRO	
268	XNDVNTPVKKRI NKL VGK -	(ILPSEFPNPLVDEAYLHPA	VDDSKOSFOWGI	POLOELRQFL	MA TVGWSKO		SPORAD13.PRO	
268	KIRPNPHDTKVKKKL -	- RTLOLTPGFPNPAAVAEAYL	KPVVDOSKGSFLWGKPOLCK	IREFCQR	YFGWNRT		HUMXPG.PRO	
268	KVAENPYDTKVKKKL -	- RKLOLT	PGFPNPAAVADAYLR	PVVDDSRGSLWGKPDVK	IREFCQR	YFGWNRM	MUSXPG.PRO	
268	KMRPNPNDTKVKKKL -	- RL	LDQOSFPNPAVASAYLKP	VVDES	KSASFSGWRPOLEO	IREFCESRF	XENXPG.PRO	
194	-----EKVYSRPHLJSTA	(LLGC	OYFORGVQNI	GIVSVFD-1	LG	FDDGN	EEDPHVILDRFASYVRE	

	360	370	380	390	400	410	420
3300	RVKHHVDKLYNLIA	-----	-----	-----	-----	-----	MJAFEN1.PRO
3314	RVKNGLERLKKA	-----	-----	-----	-----	-----	PFUFEN1.PRO
3320	RIRSGVKRLSKSRQGS	-TOGRLD	OFFKVT	-----	-----	-----	HUMFEN1.PRO
3318	RIRSGVKRLSKSRQGS	-TOGRLD	OFFKVT	-----	-----	-----	MUSFEN1.PRO
3323	RVKSGISRLKKGLKSG	-JGRLDG	FFQVV	-----	-----	-----	YST510.PRO
3335	KSDEILPLIRDVNKRKK	-----	-----	-----	-----	-----	YSTRAD2.PRO
3337	RTNEVLLPVIQDMHKKQF	-----	-----	-----	-----	-----	SPORAD13.PRO
3336	KTDESIFPVLKQLDAQTOLR	IDSFFRLA	QOEKEDAKRIKSQRL	NRAVTCMLRKEKEA	ASEIEAVSVAM	-----	HUMXPG.PRO
3336	KTDESIPVLKHLNAHOTOLR	IDSFFRLA	QOEKQODAKL(KSHRL	SRAVTCMLRKEREK	APELTKVTEAM	-----	MUSXPG.PRO
3336	KTDEVLLPVLKOLNAOOTOLR	IDSFFRLE	QHEAAG---	LKSORLRRAVTCMKR	KERDVEAEVEAAVAM	-----	XENXPG.PRO
257	EIPARSED	TORKLRLRRKKYNF	VPVGFPCND	AVHNAITMYLRPPV	SSSEIPKI	PR----	CELRAD2.PRO

FIGURE 70-D

	430	440	450	460	470	480	490
314	-	-	-	-	-	-	MJAFEN1.PRO
327	-	-	-	-	-	-	PFUFEN1.PRO
348	-	-	-	-	-	GSL	HUMFEN1.PRO
346	-	-	-	-	-	GSL	MUSFEN1.PRO
351	-	-	-	-	-	PK-T	YST51O.PRO
357	KRI NEFF	-	-	-	-	-	YSTRAD2.PRO
359	SNLT OFFEGCNTV YAPRVAYHFKSKRL ENAL SSFKNQI SNOSPMSEEIQADADAFGESKGSD ELQSRIL	-	-	-	-	-	SPORAD13.PRO
406	EKEFELL OKARKTOKRGITNTLEESSLKRKRLSOSKRKNTCGGFLGETCLSESSD GSSSEHA ESSSLM	-	-	-	-	-	HUMXPG.PRO
406	EKEFELLD AKGKTOKREL PYK-----KETSVPKRRRPSGN GGFLGD PYCSESPOESSCEDGEGSSVM	-	-	-	-	-	MUSXPG.PRO
403	ERECTNORKGOKNTKS-----QGTKRRKPTECSOEDQDPGGGFIGIELKTLSSKAYS50-----	-	-	-	-	-	XENXPG.PRO
322	MKECGWPATRTOKELALSIRRKVHLTTTV AQTRIPOFFAATKSKNF TPIVEPCESLEDYISANN-----T	-	-	-	-	-	CELRAD2.PRO

	500	510	520	530	540	550	560
314	-----	-----	-----	-----	-----	---NKTKOKTL	MJAFEN1 PRO
327	-----	-----	-----	-----	-----	---KSGKOSTL	PFUFEN1. PRO
352	SAKRKEPEPKGST	-----	-----	-----	-----	---KKKAKTGAAG	HUMFEN1. PRO
350	SAKRKEPEPKGPA	-----	-----	-----	-----	---KKKAKTGGAG	MUSFEN1. PRO
354	KEGLAAAKRAOE	-----	-----	-----	-----	---NKKLNKNKNK	YST510 PRO
364	-----	-----	---PREYISGDKKLN	TSKRISTATGKL	-----	---KK-	YSTRAD02. PRO
429	RRKMMASKNSSD	CSOSEDN	FLASLTPKTNSSS	ISIENLPRTKLSTSL	-----	---KKP	SPORAD13. PRO
476	NVORRTAAKEPK	TASDSONS	VKEAPVKN	GGATTSSSSOSDD	GGCKEMVL	VTARSVFGKRRKLR	RARGHUMXPG. PRO
469	SARQRSAAESSK	IGCSOV	PDLVROSPHGR	QGCYSTSSSD	SEDCGEOKAK	TVLTARPVFGKRRK	LKSMK-MUSXPG. PRO
458	-----	GSSSDAEDL	PSGLIDKOSQ	SVIGROKASNK	VESSSSDOED	RTVMVTAKPVFGK	KTKSKTMKEXENXPG. PRO
387	WMRKRKRSESP	O1LOHHAKR	QVPORK	-----	-----	---RSVKIRAFKPYPTOV	I CELRAD02 PRO

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FIGURE 70-E

22 DAWFKZ	MJAFEN1.PRO
35 ESWFKR	PFUFEN1.PRO
75 KFKRGK	HUMFEN1.PRO
73 KFRRGK	MUSFEN1.PRO
77 VTKGRR	YST510.PRO
90 ---RKM	YSTRAD2.PRO
83 SKRRRK	SPORAD13.PRO
46 RKRKTZ	HUMXPG.PRO
38 RRKKKT	MUSXPG.PRO
23 TVKRK	XENXPG.PRO
29 ELGDSO	CELRAD2.PRO

FIGURE 71

